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NEWS	2	AUG 10	Time limit for inactive STN sessions doubles to 40 minutes
NEWS	3	AUG 18	COMPENDEX indexing changed for the Corporate Source (CS) field
NEWS	4	AUG 24	ENCOMPLIT/ENCOMPLIT2 reloaded and enhanced
NEWS	5	AUG 24	CA/CAplus enhanced with legal status information for U.S. patents
NEWS	6	SEP 09	50 Millionth Unique Chemical Substance Recorded in CAS REGISTRY
NEWS	7	SEP 11	WPIDS, WPINDEX, and WPIX now include Japanese FTERM thesaurus
NEWS	8	OCT 21	Derwent World Patents Index Coverage of Indian and Taiwanese Content Expanded
NEWS	9	OCT 21	Derwent World Patents Index enhanced with human translated claims for Chinese Applications and Utility Models

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=> FIL BIOSIS CAPLUS EMBASE
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FULL ESTIMATED COST                                     3.30       3.30

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=> s (bend? or bent or curv?) (3a) DNA
L1       11123 (BEND? OR BENT OR CURV?) (3A) DNA

=> s matrix attachment region or scaffold attachment region or mar or
sar
L2       64211 MATRIX ATTACHMENT REGION OR SCAFFOLD ATTACHMENT REGION
OR MAR
               OR SAR

=> s l1 and l2
L3         108 L1 AND L2

=> s l3 and groove and melting temperature
L4           0 L3 AND GROOVE AND MELTING TEMPERATURE

=> s l1 and major groove and minor groove and melting temperature
L5           0 L1 AND MAJOR GROOVE AND MINOR GROOVE AND MELTING
TEMPERATURE

=> s l1 and melting temperature
L6          71 L1 AND MELTING TEMPERATURE

=> s l6 and groove
L7           3 L6 AND GROOVE

=> dup rem l7
PROCESSING COMPLETED FOR L7
L8             2 DUP REM L7 (1 DUPLICATE REMOVED)

=> d bib abs 1-
YOU HAVE REQUESTED DATA FROM 2 ANSWERS - CONTINUE? Y/(N):y

L8   ANSWER 1 OF 2  BIOSIS  COPYRIGHT (c) 2009 The Thomson
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DUPLICATE 1
AN 2002:389000 BIOSIS
DN PREV200200389000
TI Circular dichroism and thermal melting differentiation of Hoechst 33258
binding to the curved (A4T4) and straight (T4A4) DNA sequences.
AU Canzonetta, Claudia; Caneva, Roberto [Reprint author]; Savino, Maria;
Scipioni, Anita; Catalanotti, Bruno; Galeone, Aldo
CS Centro di Studio per gli Acidi Nucleici del CNR, c/o Dipartimento di
Genetica e Biologia Molecolare, Universita di Roma "La Sapienza", Piazzale
Aldo Moro. 5, 00185, Rome, Italy
roberto.caneva@uniroma1.it
SO Biochimica et Biophysica Acta, (7 June, 2002) Vol. 1576, No. 1-2, pp.
136-142. print.
CODEN: BBACAQ. ISSN: 0006-3002.
DT Article
LA English
ED Entered STN: 17 Jul 2002
Last Updated on STN: 17 Jul 2002
AB The ability of the B-DNA minor groove ligand Hoechst 33258 to
discriminate between prototype curved and straight duplex
DNA sequences was investigated by circular dichroism (CD)
titrations at the wavelengths of absorbance of the ligand. The sequences
were studied either within the framework of the ligated decamers (CA4T4G)n
and (CT4A4G)n, or within of the single dodecamers GCA4T4GC and GCT4A4GC,
to confirm and extend our earlier results based on fluorescence titrations
of ligated decamers. A unique, strong binding site is invariantly present
in both sequence units. The binding affinity of the drug for the site in
the curved A4T4 sequence was found 3- to 4-fold higher compared to the
straight sequence. All these features hold true irrespective of the
sequence framework, thus confirming that they reflect specific properties
of the binding to the two sequences. Ligand binding increases the thermal
stability of straight and curved duplex dodecamers to the same extent,
thus maintaining the melting temperature differential
between the two sequences. However, the different melting patterns and
the difference between (total ligand):(site) ratios needed for site

saturation in the two duplexes are in agreement with the difference between binding constants derived from CD measurements.

L8 ANSWER 2 OF 2 EMBASE COPYRIGHT (c) 2009 Elsevier B.V. All rights reserved on STN
AN 1996100028 EMBASE
TI Time-resolved fluorescence studies of tomaymycin bonding to synthetic DNAs.
AU Barkley, Mary D., Dr. (correspondence); Chen, Qi; Walczak, Wanda J.; Maskos, Karol
CS Department of Chemistry, Louisiana State University, Baton Rouge, LA 70808, United States. barkley@chmcafchem.lsu.edu
SO Biophysical Journal, (Apr 1996) Vol. 70, No. 4, pp. 1923-1932.
Refs: 38
ISSN: 0006-3495 CODEN: BIOJAU
CY United States
DT Journal; Article
FS 027 Biophysics, Bioengineering and Medical Instrumentation
029 Clinical and Experimental Biochemistry
LA English
SL English
ED Entered STN: 30 Apr 1996
Last Updated on STN: 30 Apr 1996
AB Tomaymycin reacts covalently with guanine in the DNA minor groove, exhibiting considerable specificity for the flanking bases. The sequence dependence of tomaymycin bonding to DNA was investigated in synthetic DNA oligomers and polymers. The maximum extent of bonding to DNA is greater for homopurine and natural DNA sequences than for alternating purine-pyrimidine sequences. Saturation of DNA with tomaymycin has little effect on the melting temperature in the absence of unbound drug. Fluorescence lifetimes were measured for DNA adducts at seven of the ten unique trinucleotide bonding sites. Most of the adducts had two fluorescence lifetimes, representing two of the four possible binding modes. The lifetimes cluster around 2-3 ns and 5-7 ns; the longer lifetime is the major component for most bonding sites. The two lifetime classes were assigned to R and S diastereomeric adducts by comparison with previous NMR results for oligomer adducts. The

lifetime difference between binding modes is interpreted in terms of an anomeric effect on the excited-state proton transfer reaction that quenches tomaymycin fluorescence. Bonding kinetics of polymer adducts were monitored by fluorescence lifetime measurements. Rates of adduct formation vary by two orders of magnitude with poly(dA-dG) .ovrhdot. poly(dC-dT), reacting the fastest at 4 x 10-2 M-1 s-1. The sequence specificity of tomaymycin is discussed in light of these findings and other reports in the literature.

=> d his

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FILE 'BIOSIS, CAPLUS, EMBASE' ENTERED AT 16:22:59 ON 21 OCT 2009
L1 11123 S (BEND? OR BENT OR CURV?) (3A) DNA
L2 64211 S MATRIX ATTACHMENT REGION OR SCAFFOLD ATTACHMENT REGION OR MAR
L3 108 S L1 AND L2
L4 0 S L3 AND GROOVE AND MELTING TEMPERATURE
L5 0 S L1 AND MAJOR GROOVE AND MINOR GROOVE AND MELTING TEMPERATURE
L6 71 S L1 AND MELTING TEMPERATURE
L7 3 S L6 AND GROOVE
L8 2 DUP REM L7 (1 DUPLICATE REMOVED)

=> dup rem l3
PROCESSING COMPLETED FOR L3
L9 56 DUP REM L3 (52 DUPLICATES REMOVED)

=> s l9 and review
L10 2 L9 AND REVIEW

=> d bib abs 1-
YOU HAVE REQUESTED DATA FROM 2 ANSWERS - CONTINUE? Y/(N):y

L10 ANSWER 1 OF 2 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2006:456032 BIOSIS
DN PREV200600447670
TI Scaffold/matrix attachment regions and intrinsic DNA curvature.
AU Fiorini, A.; Gouveia, F. de S.; Fernandez, M. A. [Reprint Author]
CS Univ Estadual Maringa, Dept Biol Celular and Genet, Av Colombo 5790,

BR-87020900 Maringa, Parana, Brazil
mafernandez@uem.br
SO Biochemistry (Moscow), (MAY 2006) Vol. 71, No. 5, pp. 481-488.
CODEN: BIORAK. ISSN: 0006-2979.
DT Article
General Review; (Literature Review)
LA English
ED Entered STN: 13 Sep 2006
Last Updated on STN: 13 Sep 2006
AB Recent approaches have failed to detect nucleotide sequence motifs in
Scaffold/Matrix Attachment Regions (S/MARs). The lack of any known
motifs, together with the confirmation that some S/MARs are not associated
to any peculiar sequence, indicates that some structural elements, such as
DNA curvature, have a role in chromatin organization and
on their efficiency in protein binding. Similar to DNA
curvature, S/MARs are located close to promoters, replication
origins, and multiple nuclear processes like recombination and breakpoint
sites. The chromatin structure in these regulatory regions is important
to chromosome organization for accurate regulation of nuclear processes.
In this article we review the biological importance of the
co-localization between bent DNA sites and S/MARs.

L10 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:574287 CAPLUS
DN 137:289445
TI Global regulation of virulence determinants in Staphylococcus aureus by
the SarA protein family
AU Cheung, Ambrose L.; Zhang, Gongyi
CS Department of Microbiology and Immunology, Dartmouth Medical School,
Hannover, NH, 03755, USA
SO Frontiers in Bioscience [online computer file] (2002), 7, D1825-D1842
CODEN: FRBIF6; ISSN: 1093-4715
URL: http://www.bioscience.org/2002/v7/d/cheung/pdf.pdf
PB Frontiers in Bioscience
DT Journal; General Review; (online computer file)
LA English
AB A review. In S. aureus, the production of virulence determinants
such as cell wall adhesins and exotoxins during the growth cycle is
controlled by global regulators such as SarA and agr. Genomic scan
reveals 16 two-component regulatory systems (e.g. agr and sae) as well as

a family of SarA homologs in S. aureus. We call the SarA homologs the SarA protein family. Many of the members in this protein family are either small basic proteins (<153 residues) or two-domain proteins in which a single domain shares sequence similarity to each of the small basic proteins. Recent crystal structures of SarR and SarA reveal dimeric structures for these proteins. Because of its structure and unique mode of DNA binding, SarR, and possibly other SarA family members, may belong to a new functional class of the winged-helix family, accommodating long stretch of DNA with bending points. AgrA. Based on sequence homol., we hypothesize that the SarA protein family may entail homologous structures with similar DNA-binding motifs but divergent activation domains. An understanding of how these regulators interact with each other in vivo and how they sense environmental signals to control virulence gene expression (e.g. α-hemolysin) will be important to our eventual goal of disrupting the regulatory network.
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=> FIL BIOSIS CAPLUS EMBASE

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                                                          ENTRY    SESSION
FULL ESTIMATED COST                                        3.71     101.58

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)              SINCE FILE      TOTAL
                                                          ENTRY    SESSION
CA SUBSCRIBER PRICE                                        0.00
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     FILE 'BIOSIS, CAPLUS, EMBASE' ENTERED AT 16:22:59 ON 21 OCT 2009
L1         11123 S (BEND? OR BENT OR CURV?) (3A) DNA
L2         64211 S MATRIX ATTACHMENT REGION OR SCAFFOLD ATTACHMENT
REGION OR MAR
L3           108 S L1 AND L2
L4             0 S L3 AND GROOVE AND MELTING TEMPERATURE
L5             0 S L1 AND MAJOR GROOVE AND MINOR GROOVE AND MELTING
TEMPERATURE
L6            71 S L1 AND MELTING TEMPERATURE
L7             3 S L6 AND GROOVE
L8             2 DUP REM L7 (1 DUPLICATE REMOVED)
L9            56 DUP REM L3 (52 DUPLICATES REMOVED)
L10            2 S L9 AND REVIEW

     FILE 'STNGUIDE' ENTERED AT 16:36:48 ON 21 OCT 2009

     FILE 'BIOSIS, CAPLUS, EMBASE' ENTERED AT 17:08:41 ON 21 OCT 2009

=> s l9 and transcript?
L11          31 L9 AND TRANSCRIPT?

=>

=> d bib abs 1-
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L11  ANSWER 1 OF 31  BIOSIS  COPYRIGHT (c) 2009 The Thomson
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AN 2007:587677 BIOSIS
DN PREV200700591083
TI Genome-wide prediction of matrix attachment regions that increase gene expression in mammalian cells.
AU Girod, Pierre-Alain; Nguyen, Duc-Quang; Calabrese, David; Puttini, Stefania; Grandjean, Melanie; Martinet, Danielle; Regamey, Alexandre; Saugy, Damien; Beckmann, Jacques S.; Bucher, Philipp; Mermod, Nicolas [Reprint Author]
CS Univ Lausanne, Inst Biotechnol, CH-1015 Lausanne, Switzerland nicolas.mermod@unil.ch
SO Nature Methods, (SEP 2007) Vol. 4, No. 9, pp. 747-753. ISSN: 1548-7091.
DT Article
LA English
OS GenBank-EF694965; EMBL-EF694965; DDJB-EF694965; GenBank-EF694966; EMBL-EF694966; DDJB-EF694966; GenBank-EF694967; EMBL-EF694967; DDJB-EF694967; GenBank-EF694968; EMBL-EF694968; DDJB-EF694968; GenBank-EF694969; EMBL-EF694969; DDJB-EF694969; GenBank-EF694970; EMBL-EF694970; DDJB-EF694970
ED Entered STN: 21 Nov 2007
Last Updated on STN: 21 Nov 2007
AB Gene transfer in eukaryotic cells and organisms suffers from epigenetic effects that result in low or unstable transgene expression and high clonal variability. Use of epigenetic regulators such as matrix attachment regions (MARs) is a promising approach to alleviate such unwanted effects. Dissection of a known MAR allowed the identification of sequence motifs that mediate elevated transgene expression. Bioinformatics analysis implied that these motifs adopt a curved DNA structure that positions nucleosomes and binds specific transcription factors. From these observations, we computed putative MARs from the human genome. Cloning of several predicted MARs indicated that they are much more potent than the previously known element, boosting the expression of recombinant proteins from cultured cells as well as mediating high and sustained expression in mice. Thus we computationally identified potent epigenetic regulators, opening new strategies toward high and stable transgene expression for research, therapeutic production or gene-based therapies.

AN 2007:315292 BIOSIS
DN PREV200700320792
TI Nuclear Dynamics: Molecular Biology and Visualization of the Nucleus.
AU Nagata, K [Editor]; Takeyasu, K [Editor]
CS Univ Tsukuba, Grad Sch Comprehens Human Sci, Dept Infect Biol, Tsukuba,
Ibaraki 3058575, Japan
SO Nagata, K [Editor]; Takeyasu, K [Editor]. (2007) Nuclear Dynamics:
Molecular Biology and Visualization of the Nucleus.
Publisher: SPRINGER, 233 SPRING STREET, NEW YORK, NY 10013, UNITED STATES.
ISBN: 978-4-431-30054-0(H).
DT Book
LA English
ED Entered STN: 24 May 2007
Last Updated on STN: 24 May 2007
AB This 279-page book discusses nuclear dynamics, focusing on molecular
biology and visualization of the nucleus. The book begins with an
overview of nuclear organization and nuclear dynamics. The remainder of
the book is structured into 15 individually-authored chapters. Chapter 1
discusses visual biology of nuclear dynamics from micro- to nano-dynamics
of nuclear components, and chapter 2 focuses on the nuclear envelope.
Topics covered in chapters 3-9 include, respectively: mitotic chromosome
segregation control; breakdown and reformation of the nuclear envelope;
functional organization and dynamic aspects of nucleoli during the cell
cycle; dynamics, roles, and diseases of the nuclear membrane, lamins, and
lamin-binding proteins; gene selectors consisting of DNA-binding proteins,
histones, and histone-binding proteins and regulation of the 3 major
stages of gene expression; dynamic chromatin loops and the regulation of
gene expression; and topology and function of chromatin and non-chromatin
nuclear dynamics. Remaining chapter topics include: regulation of
chromatin structure by curved DNA and how activator
sites become accessible; actin-related proteins involved in nuclear and
chromatin dynamics; effects of 5-bromodeoxyuridine on chromatin structure;

transcriptional modulation by nuclear matrix protein P130/MAT3 associated with MAR/SAR; and breaking and tessellating the contiguous nuclear genome. The book finishes with a perspective on understanding in situ genome function. The text is written in English.
The book is illustrated with 48 figures, 34 of which are in color. This book will serve as an invaluable source of reference for researchers in the areas of cell biology, molecular biology, molecular genetics, and developmental biology.

L11 ANSWER 3 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2007:180217 BIOSIS
DN PREV200700174447
TI Avian lysozyme promoter.
AU Anonymous; Rapp, Jeffrey C. [Inventor]
CS Athens, GA USA
ASSIGNEE: AviGenics Inc
PI US 07176300 20070213
SO Official Gazette of the United States Patent and Trademark Office Patents,
(FEB 13 2007)
CODEN: OGUPE7. ISSN: 0098-1133.
DT Patent
LA English
ED Entered STN: 7 Mar 2007
Last Updated on STN: 7 Mar 2007
AB The invention provides for lysozyme gene expression control regions which may include a 5 ' matrix attachment region; an intrinsically curved region of DNA; a transcription enhancer; a negative regulatory element; at least one hormone responsive element; an avian CRI repeat element; a proximal lysozyme promoter, and can be linked to a nucleotide sequence encoding a heterologous polypeptide.

L11 ANSWER 4 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2006:479327 BIOSIS
DN PREV200600464482
TI Multiple initiation sites within the human ribosomal RNA gene.
AU Coffman, Frederick D. [Reprint Author]; He, Mai; Diaz, Mai-Ling; Cohen, Stanley
CS Univ Med and Dent New Jersey, New Jersey Med Sch, Dept Pathol and Lab Med,

MSB C569,185 S Orange Ave, Newark, NJ 07103 USA
coffmafd@umdnj.edu
SO Cell Cycle, (JUN 1 2006) Vol. 5, No. 11, pp. 1223-1233.
ISSN: 1538-4101.
DT Article
LA English
ED Entered STN: 20 Sep 2006
Last Updated on STN: 20 Sep 2006
AB Numerous studies have demonstrated that DNA replication initiates within the 30 kB non-transcribed spacer (NTS) region of the human ribosomal RNA gene (rDNA). Using a series of closely spaced primer pairs to measure nascent leading strand abundance in mid and late S phase cells isolated by centrifugal elutriation, we find evidence for one highly preferred initiation site and two less utilized sites within a 6 kb region of the NTS. The initiation sites colocalize with significant DNA unwinding elements (DUEs), matrix attachment regions (MARs), and ARS-like sequences. An intrinsic DNA bending site was localized by circular permutation analysis to within several hundred base pairs of one initiation site. While DUE and MAR elements occur elsewhere throughout the 43 kb rDNA sequence, the close association of DUE and MAR elements occurs only near replication initiation sites, a juxtaposition also seen in other well-studied mammalian replication initiation sites. The utilization of rDNA initiation sites close to DUE and MAR elements in mid and late S phase, but not in very early S phase as previously shown, suggests that in rRNA genes, contributions from these sequence-associated properties may be more significant to initiation sites associated with transcriptionally inactive genes, than to initiation sites associated with transcriptionally active genes.

L11 ANSWER 5 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2006:447473 BIOSIS
DN PREV200600456099
TI DNA bending in the replication zone of the C3 DNA puff amplicon of Rhynchosciara americana (Diptera : Sciaridae).
AU Fiorini, Adriana; de Souza Gouveia, Fabiana; Albertina de Miranda Soares,

Maria; Stocker, Ann Jacob; Ciferri, Ricardo Rodrigues; Fernandez, Maria
Aparecida [Reprint Author]
CS Univ Estadual Maringa, Dept Biol Celular and Genet, Av Colombo 5790,
BR-87020900 Maringa, Parana, Brazil
mafernandez@uem.br
SO Molecular Biology Reports, (MAR 2006) Vol. 33, No. 1, pp. 71-82.
CODEN: MLBRBU. ISSN: 0301-4851.
DT Article
LA English
ED Entered STN: 13 Sep 2006
Last Updated on STN: 13 Sep 2006
AB Intrinsic bent DNA sites were identified in the 4289
bp segment encompassing the replication zone which directs DNA
amplification and transcription of the C3-22 gene of
Rhynchosciara americana. Restriction fragments showed reduced
electrophoretic mobility in polyacrylamide gels. The 2D modeling of the
3D DNA path and the ENDS ratio values obtained from the dinucleotide wedge
model of Trifonov revealed the presence of four major bent sites,
positioned at nucleotides -6753, -5433, -5133 and -4757. Sequence
analysis showed that these bends are composed of 2-6 bp dA(.)dT tracts in
phase with the DNA helical repeat. The circular permutation analysis
permitted the verification that the fragments containing the bending sites
promote curvature in other sequence contexts. Computer analyses of the
4289 bp sequence revealed low helical stability (Delta G values), negative
roll angles indicating a narrow minor groove and a putative matrix
attachment region. The data presented in this paper add
to information about the structural features involved in this amplified
segment.

L11 ANSWER 6 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2004:115753 BIOSIS
DN PREV200400116434
TI Multiple cis-acting sequences implicate function diversity in nuclear
matrix attachment regions of bovine mammary gland.
AU Lao Wei-De [Reprint Author]; Zhang Chuan-Sheng [Reprint Author]; Hu Guo-Fa
[Reprint Author]; Zhang Xu-Chen [Reprint Author]; Wei Ying-Yun [Reprint

Author]
CS Institute of Genetics and Developmental Biology, Chinese Academy of
Sciences, Beijing, 100080, China
SO Acta Genetica Sinica, (May 2003) Vol. 30, No. 5, pp. 397-406. print.
ISSN: 0379-4172 (ISSN print).
DT Article
LA English
ED Entered STN: 3 Mar 2004
Last Updated on STN: 3 Mar 2004
AB Chromosomal DNA in higher eukaryotes is spatially organized into loops by
periodic attachment to the nuclear matrix at its base via a specific
matrix attachment region (MAR). In
order to study the nature of DNA sequences that affixed the loops to the
nuclear matrix, we have cloned the MAR DNA from bovine lactating
mammary tissues. In vitro binding assay showed that the cloned fragments
could be co-complexed with nuclear matrix proteins to form insoluble
complex easily removed by centrifugation. Sequences of the two chosen
MAR loci are composed of TG-, CA- and GA- blocks, as well as the
ATTA motifs. Both the MAR loci show numerous replication/
transcription factor binding sites, enhancer motifs, several
perfect or imperfect inverted repeats, and sequences sharing the common
features of the potential DNA bending core sequence.
The possibility that a combination of different elements in the same DNA
sequence may function as either positive or negative regulatory elements
in controlling a variety of cellular and developmental processes is
discussed.

L11 ANSWER 7 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2003:330192 BIOSIS
DN PREV200300330192
TI Interaction in vitro of type III intermediate filament proteins with Z-DNA
and B-Z-DNA junctions.
AU Li, Guohong; Tolstonog, Genrich V.; Traub, Peter [Reprint Author]
CS Max-Planck-Institut fuer Zellbiologie, Rosenhof, 68526, Ladenburg, Germany
ptraub@zellbio.mpg.de
SO DNA and Cell Biology, (March 2003) Vol. 22, No. 3, pp. 141-169. print.

ISSN: 1044-5498 (ISSN print).
DT Article
LA English
ED Entered STN: 16 Jul 2003
Last Updated on STN: 16 Jul 2003
AB The selection of DNA fragments containing simple d(GT)n and composite
d(GT)mcntdotd(GA)n microsatellites during affinity binding of mouse
genomic DNA to type III cytoplasmic intermediate filaments (cIFs) in
vitro, and the detection of such repeats, often as parts of nuclear
matrix attachment region (MAR)-like
DNA, in SDS-stable DNA-vimentin crosslinkage products isolated from intact
fibroblasts, prompted a detailed study of the interaction of type III cIF
proteins with left-handed Z-DNA formed from d(GT)17 and d(CG)17 repeats
under the topological tension of negatively supercoiled plasmids.
Although d(GT)n tracts possess a distinctly lower Z-DNA-forming potential
than d(CG)n tracts, the filament proteins produced a stronger
electrophoretic mobility shift with a plasmid carrying a d(GT)17 insert
than with plasmids containing different d(CG)n inserts, consistent with
the facts that the B-Z transition of d(GT)n repeats requires a higher
negative super-helical density than that of d(CG)n repeats and the
affinity of cIF proteins for plasmid DNA increases with its superhelical
tension. That both types of dinucleotide repeat had indeed undergone B-Z
transition was confirmed by S1 nuclease and chemical footprinting analysis
of the plasmids, which also demonstrated efficient protection by cIF
proteins from nucleolytic and chemical attack of the Z-DNA helices as
such, as well as of the flanking B-Z junctions. The analysis also
revealed sensibilization of nucleotides in the center of one of the two
strands of a perfect d(CG)17 insert toward S1 nuclease, indicating cIF
protein-induced bending of the repeat. In all these assays, vimentin and
glial fibrillary acidic protein (GFAP) showed comparable activities,

versus desmin, which was almost inactive. In addition, vimentin and GFAP exhibited much higher affinities for the Z-DNA conformation of brominated, linear d(CG)25 repeats than for the B-DNA configuration of the unmodified oligonucleotides. While double-stranded DNA was incapable of chasing the Z-DNA from its protein complexes, and Holliday junction and single-stranded (ss)DNA were distinguished by reasonable competitiveness, phosphatidylinositol (PI) and, particularly, phosphatidylinositol 4,5-diphosphate (PIP2) turned out to be extremely potent competitors. Because PIP2 is an important member of the nuclear PI signal transduction cascade, it might exert a regulatory influence on the binding of cIF proteins to Z- and other DNA conformations. From this interaction of cIF proteins with Z- and bent DNA and their previously detected affinities for MAR-like, ss, triple helical, and four-way junction DNA, it may be concluded that the filament proteins play a general role in such nuclear matrix-associated processes as DNA replication, recombination, repair, and transcription.

L11 ANSWER 8 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2002:560852 BIOSIS
DN PREV200200560852
TI A comprehensive alanine scanning mutagenesis of the Escherichia coli transcriptional activator SoxS: Identifying amino acids important for DNA binding and transcription activation.
AU Griffith, Kevin L.; Wolf, Richard E., Jr. [Reprint author]
CS Department of Biological Sciences, University of Maryland Baltimore County, 1000 Hilltop Circle, Baltimore, MD, 21250, USA wolf@umbc.edu
SO Journal of Molecular Biology, (13 September, 2002) Vol. 322, No. 2, pp. 237-257. print. CODEN: JMOBAK. ISSN: 0022-2836.
DT Article
LA English
ED Entered STN: 30 Oct 2002 Last Updated on STN: 30 Oct 2002
AB SoxS is the direct transcriptional activator of the superoxide regulon. SoxS recognizes a highly degenerate "soxbox" DNA sequence, and activates transcription from class I and class II promoters.

SoxS is the smallest member of the AraC/XylS family of transcription regulators whose hallmark is dual helix-turn-helix (HTH) DNA-binding motifs. Evidence suggests that the N-terminal HTH motif of SoxS interacts with a highly conserved region of the soxbox termed recognition element 1 (RE1), while the C-terminal HTH motif interacts with the less conserved recognition element 2 (RE2). In the work described here, we prepared a complete library of 101 SoxS mutants containing single alanine substitutions of SoxS, and we characterized the mutant proteins in vivo and in vitro. With SoxS being closely related to MarA, we analyzed the effects of the SoxS mutations in the context of the MarA-mar crystal structure and with respect to the NMR study of MarA-DNA complexes in solution. From the properties of the alanine substitutions, we conclude the following. (1) Surface-exposed residues of helix 3 and helix 6, the recognition helices of the dual HTH motifs, are important to DNA binding and transcription activation; however, substitutions of residues predicted from the MarA-mar crystal structure to make contact with the sugar-phosphate backbone are more detrimental to DNA binding than mutations predicted to make base-specific contacts. (2) Substitution of several residues within the recognition helix predicted to make base-specific contacts with RE2 have relatively little effect on DNA-binding, suggesting the possibility of alternative protein-DNA interactions than those inferred from the MarA-mar crystal structure. (3) DNA binding and transcription activation were reduced by substitution of conserved amino acid residues comprising the hydrophobic core, presumably because they disrupt the structural integrity of SoxS. (4) Mutant K30A appears to be a positive control mutant defective in a protein-protein interaction with RNA polymerase that is required for transcription activation at all SoxS-dependent promoters because it binds and bends DNA normally but fails to activate transcription from both classes of promoters. Alanine substitutions of surface-exposed residues H3, K5, D9, S31, and V45 confer

a similar phenotype. Since these residues are near K30 on the surface of the protein, the surface formed by the six residues may be used to make protein-protein interactions with RNA polymerase that are required for transcription activation at both class I and class II SoxS-dependent promoters. (5) Mutants F74A, D75A, M78A, D79A and Q85A appear to define a surface required for protein-protein interaction with RNA polymerase specifically at class II promoters because these positive control mutants bind and bend DNA normally but are defective in activation of class II promoters but not class I promoters. These SoxS mutants that bind and bend DNA normally but are defective in transcription activation represent the first positive control mutants with putative defects in protein-protein interactions with RNA polymerase among the SoxS/MarA/Rob subset of the AraC/XylS family of transcription regulators.

L11 ANSWER 9 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 2001:354458 BIOSIS
DN PREV200100354458
TI Crystal structure of the SarR protein from Staphylococcus aureus.
AU Liu, Yingfang; Manna, Adhar; Li, Ronggui; Martin, Wesley E.; Murphy, Robert C.; Cheung, Ambrose L.; Zhang, Gongyi [Reprint author]
CS 1400 Jackson Street, 501b, Denver, CO, 80206, USA
zhangg@njc.org
SO Proceedings of the National Academy of Sciences of the United States of America, (June 5, 2001) Vol. 98, No. 12, pp. 6877-6882. print.
CODEN: PNASA6. ISSN: 0027-8424.
DT Article
LA English
ED Entered STN: 2 Aug 2001
Last Updated on STN: 19 Feb 2002
AB The expression of virulence determinants in Staphylococcus aureus is controlled by global regulatory loci (e.g., sarA and agr). The sar (Staphylococcus accessory regulator) locus is composed of three overlapping transcripts (sarA P1, P3, and P2, transcripts initiated from the P1, P3, and P2 promoters, respectively), all encoding the 124-aa SarA protein. The level of SarA, the major regulatory protein, is partially controlled by the differential

activation of the sarA promoters. We previously partially purified a 13.6-kDa protein, designated SarR, that binds to the sarA promoter region to down-modulate sarA transcription from the P1 promoter and subsequently SarA expression. SarR shares sequence similarity to SarA, and another SarA homolog, SarS. Here we report the 2.3 ANG-resolution x-ray crystal structure of the dimeric SarR-MBP (maltose binding protein) fusion protein. The structure reveals that the SarR protein not only has a classic helix-turn-helix module for DNA binding at the major grooves, but also has an additional loop region involved in DNA recognition at the minor grooves. This interaction mode could represent a new functional class of the "winged helix" family. The dimeric SarR structure could accommodate an unusually long stretch of apprxeq27 nucleotides with two or four bending points along the course, which could lead to the bending of DNA by 90degree or more, similar to that seen in the catabolite activator protein (CAP)-DNA complex. The structure also demonstrates the molecular basis for the stable dimerization of the SarR monomers and possible motifs for interaction with other proteins.

L11 ANSWER 10 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN

AN 2001:49609 BIOSIS

DN PREV200100049609

TI Interaction of nuclear proteins with intrinsically curved DNA in a matrix attachment region of a tobacco gene.

AU Fukuda, Yuji [Reprint author]

CS Plant Molecular Biology Laboratory, Molecular Biology Department, National Institute of Bioscience and Human Technology, AIST, MITI, Higashi 1-1, Tsukuba, Ibaraki, 305-8566, Japan
yfukuda@nibh.go.jp

SO Plant Molecular Biology, (September, 2000) Vol. 44, No. 1, pp. 91-98.
print.
CODEN: PMBIDB. ISSN: 0167-4412.

DT Article

LA English

ED Entered STN: 24 Jan 2001
Last Updated on STN: 12 Feb 2002
AB Two scaffold/matrix attachment regions (S/MARs), designated S/M I and S/M
II, are located in the 5'-flanking region of the tobacco basic class I
chitinase gene, CHN50. Structural analysis of these S/MARs showed that
S/M II contained an intrinsically curved DNA sequence
that is located between -1786 and -1722 relative to the initiation site of
transcription. Electrophoretic mobility shift assays and
southwestern blotting analysis were performed to identify the tobacco
nuclear proteins that bind specifically to this curved
DNA. These experiments revealed that nuclear proteins bound
specifically to the curved DNA. Moreover, the nuclear
proteins appeared to recognize the overall structure of the intrinsically
curved DNA, as distinct from binding to the DNA with
sequence specificity. Southwestern blotting analysis showed that proteins
of 22, 24, 28 and 34 kDa bound specifically to the curved
DNA. The possible functions of the binding proteins and their
relationship to previously identified nuclear proteins, such as
high-mobility-group proteins, are discussed.

L11 ANSWER 11 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN
AN 1999:263746 BIOSIS
DN PREV199900263746
TI Characterization of matrix attachment sites in the upstream region of a
tobacco chitinase gene.
AU Fukuda, Yuji [Reprint author]
CS Plant Molecular Biology Laboratory, Molecular Biology Department, National
Institute of Bioscience and Human Technology, AIST, MITI, Higashi 1-1,
Tsukuba, Ibaraki, 305-8566, Japan
SO Plant Molecular Biology, (March, 1999) Vol. 39, No. 5, pp. 1051-1062.
print.
CODEN: PMBIDB. ISSN: 0167-4412.
DT Article
LA English
OS Genbank-AJ006034; EMBL-AJ006034; DDBJ-AJ006034
ED Entered STN: 15 Jul 1999
Last Updated on STN: 15 Jul 1999
AB The nuclear matrix is thought to partition the genome into functional and

structural loop domains, and it has been implicated in several cellular processes, such as the replication and transcription of DNA and the processing of RNA. Therefore, the analysis of scaffold/matrix-associated DNA regions (S/MARs) might enhance our understanding of the functional roles of the higher-order organization of chromatin. In this study, the upstream region between positions -3320 and -1095 of the basic class I chitinase gene, CHN50, was shown to have specific affinity for the tobacco nuclear scaffold. Detailed analysis of nuclear scaffold-DNA binding in vitro revealed that two regions (positions -3320 to -2621 and -2221 to -1371) bound specifically to the nuclear scaffold. These S/MAR elements, designated S/M I and S/M II, are A+T-rich sequences with 75% and 74% A+T residues, respectively, and may include a number of sequence motifs that have frequently been found in other S/MARs. Moreover, S/M II contains a curved DNA sequence with anomalous mobility on polyacrylamide gels. A circular permutation assay revealed that the center of this curved region was located between positions -1767 and -1759. The possible functions and structural features of the S/MAR elements in the upstream region of CHN50 are discussed.

L11 ANSWER 12 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1998:32304 BIOSIS
DN PREV199800032304
TI Fis, and accessorial factor for transcriptional activation of the mar (multiple antibiotic resistance) promoter of Escherichia coli in the presence of the activator MarA, SoxS, or Rob.
AU Martin, Robert G. [Reprint author]; Rosner, Judah L.
CS Bldg. 5, Room 333, NIH, Bethesda, MD 20892-0560, USA
SO Journal of Bacteriology, (Dec., 1997) Vol. 179, No. 23, pp. 7410-7419.
print.
CODEN: JOBAAY. ISSN: 0021-9193.
DT Article
LA English
ED Entered STN: 14 Jan 1998
Last Updated on STN: 14 Jan 1998
AB Transcription of the multiple antibiotic resistance marRAB operon increases when one of the sequence-related activators, MarA, SoxS,

or Rob, binds to the "marbox" centered at -61.5 relative to the transcriptional start site. Previous deletion analyses showed that an adjacent upstream "accessory region" was needed to augment the marbox-dependent activation. To analyze the roles of the marbox and accessory regions on mar transcription, thirteen promoters, each with a different 5-bp transversion of the -96 to -32 sequence, were synthesized, fused to lacZ, and assayed for beta-galactosidase production in single-copy lysogens with appropriate genotypes. The accessory region is shown here to be a binding site for Fis centered at -81 and to bind Fis, a small DNA-binding and -bending protein, with a Kd of apprxeq5 nM. The binding of MarA to the marbox and that of Fis to its site were independent of each other. MarA, SoxS, and Rob each activated the mar promoter 1.5- to 2-fold when it had a wild-type marbox but Fis was absent. In the presence of MarA, SoxS, or Rob, Fis further enhanced the activity of the promoter twofold provided the promoter was also capable of binding Fis. However, in the absence of MarA, SoxS, or Rob or in the absence of a wild-type marbox, Fis nonspecifically lowered the activity of the mar promoter about 25% whether or not a wild-type Fis site was present. Thus, Fis acts as an accessory transcriptional activator at the mar promoter.

L11 ANSWER 13 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1997:22480 BIOSIS
DN PREV199799321683
TI The 3' untranslated region of the human poly(ADP-ribose) polymerase gene is a nuclear matrix anchoring site.
AU Boulikas, Teni [Reprint author]; Kong, C. F.; Brooks, Down; Hsie, Linda
CS Inst. Molecular Med. Sci., 460 Page Mill Road, Palo Alto, CA 94306, USA
SO International Journal of Oncology, (1996) Vol. 9, No. 6, pp. 1287-1294.
ISSN: 1019-6439.
DT Article
LA English
ED Entered STN: 15 Jan 1997

Last Updated on STN: 23 Jan 1997
AB The nuclear matrix displays the most dramatic changes among all cellular structures during carcinogenesis. Matrix attachment regions (MARs) organize chromatin into domains, harbor origins of replication and display a notable transcriptional enhancer activity. To understand the nature of MARs and their involvement in gene expression, replication, and carcinogenesis, we have cloned the MAR DNA fragments, of a size of 0. 1-5.0 kb, isolated from human cells in culture. Over 150 clones have been sequenced. One MAR clone was identified as a stretch of 393 hp from the 3' untranslated region (3' UTR) of the human poly(ADP-ribose) polymerase (PARP) gene (100% homology). The 393 bp MAR fragment contains several repeats of TTGTTTTGT and related sequences (the TG boxes) and motifs with similarity to the binding site of the general yeast transcription factor GFI and to the ARS origins of replication in yeast. In addition, the 3' UTR of the PARP gene harbors MAR-type sequences found in other genes, kinked and curved DNA, two imperfect inverted repeats, and short alternating GA- and CT-rich motifs. The presence of TG-, GA-, and CT-rich motifs and of potential cruciforms is proposed to identify a novel type of MAR sequence. This report suggests that MAR sequences may reside in the 3' untranslated region of other genes and has important implications for a potential role of the nuclear matrix in transcription termination.

L11 ANSWER 14 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1996:282661 BIOSIS
DN PREV199699005017
TI Transcriptional activation of promoters of the superoxide and multiple antibiotic resistance regulons by Rob, a binding protein of the Escherichia coli origin of chromosomal replication.
AU Jair, Kam-Wing; Yu, Xin; Skarstad, Kirsten; Thony, Beat; Fujita, Nobuyuki; Ishihama, Akira; Wolf, Richard E., Jr. [Reprint author]
CS Dep. Biol. Sci., Univ. Maryland Baltimore County, Baltimore, MD 21228, USA
SO Journal of Bacteriology, (1996) Vol. 178, No. 9, pp. 2507-2513. CODEN: JOBAAY. ISSN: 0021-9193.
DT Article

LA English
ED Entered STN: 25 Jun 1996
Last Updated on STN: 25 Jun 1996
AB The Rob protein, isolated on the basis of its ability to bind to the right arm of the Escherichia coli origin of chromosomal replication, is about 50% identical in amino acid sequence to SoxS and MarA, the direct regulators of the superoxide (soxRS) and multiple antibiotic resistance (mar) regulons, respectively. Having previously demonstrated that SoxS (as a MalE-SoxS fusion protein) and MarA are essentially identical in their abilities to activate in vitro transcription of genes of the sox-mar regulons, we investigated the properties of Rob as a transcriptional activator. We found that Rob (i) activates the transcription of zwf,fpr,fumC, micF, nfo, and sodA, (ii) requires a 21-bp soxbox-marbox-robbox sequence to activate zwf transcription, (iii) protects the soxbox/marbox/robbox from attack by DNase 1, (iv) is ambidextrous, i.e., requires the C-terminal domain of the alpha subunit of RNA polymerase for activation of zwf but not fumC or micF, (v) bends zwf and fumC DNA, and (vi) binds zwf and fumC DNA as a monomer. Since these transcription activation properties of Rob are virtually identical to those of MalE-SoxS and MarA, it appears as if the E. coli genome encodes three genes with the same functional capacity. However, in contrast to SoxS and MarA, whose syntheses are induced by specific environmental stimuli and elicit a clear defense response, Rob is expressed constitutively and its normal function is unknown.

L11 ANSWER 15 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1996:219547 BIOSIS
DN PREV199698775676
TI Common structural features of replication origins in all life forms.
AU Boulikas, Teni
CS Inst. Molecular Med. Sci., Palo Alto, CA 94306, USA
SO Journal of Cellular Biochemistry, (1996) Vol. 60, No. 3, pp. 297-316.
CODEN: JCEBD5. ISSN: 0730-2312.
DT Article
General Review; (Literature Review)

LA English
ED Entered STN: 8 May 1996
Last Updated on STN: 8 May 1996
AB Origins of replication (ORIs) among prokaryotes, viruses, and multicellular organisms appear to possess simple tri-, tetra-, or higher dispersed repetitions of nucleotides, AT tracts, inverted repeats, one to four binding sites of an initiator protein, intrinsically curved DNA, DNase I-hypersensitive sites, a distinct pattern of DNA methylation, and binding sites for transcription factors. Eukaryotic ORIs are sequestered on the nuclear matrix; this attachment is supposed to facilitate execution of their activation/deactivation programs during development. Furthermore, ORIs fall into various classes with respect to their sequence complexity: those enriched in AT tracts, those with GA- and CT-rich tracts, a smaller class of GC-rich ORIs, and a major class composed of mixed motifs yet containing distinct AT and polypurine or GC stretches. Multimers of an initiator protein in prokaryotes and viruses that might have evolved into a multiprotein replication initiation complex in multicellular organisms bind to the core ORI, causing a structural distortion to the DNA which is transferred to the AT tract flanking the initiator protein site; single-stranded DNA-binding proteins then interact with the melted AT tract as well as with the DNA polymerase a-primase complex in animal viruses and mammalian cells, causing initiation in DNA replication. ORIs in mammalian cells seem to colocalize with matrix-attached regions and are proposed to become DNase I-hypersensitive during their activation.

L11 ANSWER 16 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1996:165022 BIOSIS
DN PREV199698737157
TI Anatomy of highly expressing chromosomal sites targeted by retroviral vectors.
AU Mielke, Christian; Maass, Karin; Tuemmler, Meike; Bode, Juergen [Reprint author]

CS GBF, Gesellschaft Biotechnol. Forschung mbH, Genregulation Differenzierung/Genetik von Eukaryonten, Mascheroder Weg, D-38124 Braunschweig, Germany
SO Biochemistry, (1996) Vol. 35, No. 7, pp. 2239-2252.
CODEN: BICHAW. ISSN: 0006-2960.
DT Article
LA English
ED Entered STN: 11 Apr 1996
Last Updated on STN: 11 Apr 1996
AB The eukaryotic genome contains chromosomal loci with a high transcription-promoting potential. For their identification in cultured cells, transfer of a retroviral vectors in conjunction with that grants the integration of individual copies. We have applied retroviral vectors in conjunction with inverse polymerase chain reaction techniques to reconstruct a number of these sites for a further characterization.
Remarkably, all examples conform to the same design in that the process of retroviral infection selected a scaffold- or matrix-attached region (S/MAR) that was flanked by DNA with high bending potential. The S/MARs are of an unusual type in that they show a high incidence of certain dinucleotide repeats and the potential to act as topological sinks. The anatomy of retroviral integration sites reveals principles that can be exploited for the development of predictable transgenic systems on the basis of expression and targeting vectors.

L11 ANSWER 17 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1994:449236 BIOSIS
DN PREV199497462236
TI Transcription factor binding sites in the matrix attachment region (MAR) of the chicken alpha-globin gene.
AU Boulikas, Teni
CS Inst. Molecular Med. Sci., 460 Page Mill Road, Palo Alto, CA 94306, USA
SO Journal of Cellular Biochemistry, (1994) Vol. 55, No. 4, pp. 513-529.
CODEN: JCEBD5. ISSN: 0730-2312.
DT Article
LA English
ED Entered STN: 24 Oct 1994

Last Updated on STN: 24 Oct 1994

AB Nuclear matrix is a nuclear protein-DNA superstructure believed to be the exclusive site of DNA replication, transcription, repair, and recombination. The attachment regions of chromatin loops to the nuclear matrix, called MARs, nest origins of replication, have transcriptional enhancer activity, and via their interaction with protein transcription factors may govern gene switch during development and tissue-specific gene expression. In this study the 967 bp MAR of the chicken alpha-globin gene is analyzed for the presence of hexanucleotides from a number (83 in total) of vertebrate protein transcription factors and core origins of replication. A total number of 760 hexanucleotides from factor sites or origins of replication were used for this search. We found that: (1) The occurrence of protein transcription factor binding sites overall on the MAR fragment as well as on the enhancer and promoter regions of other genes is only about 1.2-1.5 times higher than in random DNA, something consistent for all MAR and enhancer sequences examined. However, a high concentration (up to 2.7 times over random sequences) of hexanucleotide factor sites is observed on small stretches of the alpha-globin gene MAR. (2) Some regulatory protein binding sites are underrepresented whereas others are overrepresented, giving to an MAR a particular transcription factor flavor. (3) The DNA curvature map of the MAR sequence and the potential sites of positioned nucleosomes suggest the sites where a competition between core histone octamers and protein transcription factors for DNA might be found. This approach might provide a novel technique to diagnose for the regulatory or nonregulatory function of a stretch of DNA. Furthermore, MARs are proposed to constitute important regulatory elements of genes in addition to enhancers, promoters, silencers, locus control regions, and origins of replication. Additional parameters such as interaction of a transcription factor with other transcription factors fixed at vicinal sites, DNA methylation, intrinsic DNA curvature torsional strain, and nucleosome positioning might also determine the high-affinity binding of a transcription factor to its functional sites and its exclusion from or low affinity binding to other nonregulatory regions.

L11 ANSWER 18 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN
AN 1993:522833 BIOSIS
DN PREV199396136240
TI CDNA clones contain autonomous replication activity.
AU Wu, Cunle; Friedlander, Paula; Lamoureux, Claude; Zannis-Hadjopoulos,
Maria; Price, Gerald B. [Reprint author]
CS McGuill Cancer Cent., Room 707, 3655 Drummond Street, Montreal, PQ H3G
1Y6, Canada
SO Biochimica et Biophysica Acta, (1993) Vol. 1174, No. 3, pp. 241-257.
CODEN: BBACAQ. ISSN: 0006-3002.
DT Article
LA English
ED Entered STN: 19 Nov 1993
Last Updated on STN: 3 Jan 1995
AB We have undertaken to investigate transcription as a regulatory
event in mammalian DNA replication. Subpopulations of transcripts
represented in a cDNA library of human embryo lung fibroblasts (IMR90)
were examined for their ability to support autonomous replication after
transfection into human cells (HeLa). Two of three cDNA clones (343, 363)
containing "O"-family repetitive sequences, after subcloning into pBR322
and transfection into HeLa cells, were capable of autonomous replication.
One of these cDNA clones, 343, is enriched by selection for poly(A)+ RNA.
In contrast, none of five Alu-containing transcripts was capable
of autonomous replication in human cells. However, six out of ten cDNA
clones contained neither "O"-family or Alu homologous sequences and were
as efficient as the cDNA clones containing "O"-family sequences in
replicating autonomously in human cells. cDNA clones, from an
oligo-d(T)-primed library of human poly(A)+ enriched RNA, contain a
significant proportion of independent clones that can also support
autonomous replication of bacterial plasmids in human cells. cDNA clone
343 was observed to contain in a 448 bp EcoRI-HincII fragment, yeast ARS
consensus, SAR consensus, IRs, bent DNA and

a DUE, all sequence and structural characteristics often associated with many prokaryotic, viral and eukaryotic origins. Sequence analysis of seven other cDNA clones (from non-'O'-family, non-Alu homologous sequences, NOA) showed that five contained some of the same consensus sequences. Two NOA clones (NOA4 and -5) did not contain any representations of ARS and SAR consensus sequences, suggesting that these two features may not be essential for autonomous replication activity in mammalian cells.

L11 ANSWER 19 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
AN 1993:365699 BIOSIS
DN PREV199396051374
TI Nature of DNA sequences at the attachment regions of genes to the nuclear matrix.
AU Boulikas, Teni
CS Inst. Molecular Med. Sciences, 460 Page Mill Road, Palo Alto, CA 94306, USA
SO Journal of Cellular Biochemistry, (1993) Vol. 52, No. 1, pp. 14-22.
CODEN: JCEBD5. ISSN: 0730-2312.
DT Article
LA English
ED Entered STN: 6 Aug 1993
Last Updated on STN: 6 Aug 1993
AB Matrix-attached regions (MARs) have been demonstrated to nest origins of replication and transcriptional enhancers. A set of 13 rules is proposed aimed at facilitating the classification of a DNA sequence as a matrix attachment regions. These rules, which were deduced from a study of known MARs from other genes and some others identified in our laboratory, are (1) potential origin of replication are MARs; (2) the major class of MARs seclude clusters of AT-rich motifs and may harbor topoisomerase II binding and cleavage sites; (3) the AT-rich class of MARs may comprise the DNA sequence motifs ATTA and ATTTA representing core binding sites of homeotic proteins, implying the MARs may participate in the differential activation of origins of replication and in gene switch during development; (4) the habitat of MARs may include mass binding sites for protein transcription factors; even weak factor binding sites may lead to

the formation of tight protein-DNA supramolecular structures; (5) MARs may contain intrinsically curved DNA; one type is oligo(dA) stretches of 3 to 7 nucleotides spaced every 10.5 nucleotides; (6) a class of MARs may contain kinked DNA, formed by CA, TG, and TA dinucleotides at distances of 5 to 10.5 nucleotides from their centres; the same dinucleotides, known to be abundant in protein recognition sites, may be overrepresented in a special class of MARs; (7) the AT-rich core of MARs may be flanked, at one or both sides, by sequences that can adopt the left-handed or triple-helical DNA structure; these include TG, TA, GC repeats and polypurine or polypyrimidine stretches; (8) palindromic (dyad symmetry) sequences, able to form cruciform structures when the DNA is under torsional strain may be found within MARs, and more so when the MAR is also an origin of replication; (9) transcriptional enhancers may be MARs; (10) a class of MARs may be composed of stretches of GA-rich DNA alternating with CT-rich stretches, 5-50 nucleotides long; (11) a class of MARs may be enriched in TG bones, usually 6-12 nucleotides long, such as TGTTTTGGGG; this type of MAR occurs in the 3'-untranslated region of several genes, builds up to chromosome telomeres, and is highly recombinogenic; (12) a small fraction of Alu sequences might have MAR activity. This might depend on the number and distance from one another of DNA sequence motifs representing protein binding sites; and (13) MARs may coincide with the DNAse I hypersensitive sites of chromatin. It is proposed here that MAR sequence can provide markers for mapping and sequencing the human, and other, genomes. Furthermore, it is proposed that large scale random cloning of MARs might advance our knowledge on the nature of DNA sequences that are used for the initiation of DNA replication, as transcriptional enhancers and as borders between chromatin domains.

L11 ANSWER 20 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN

AN 2008:253136 CAPLUS
DN 148:301029
TI Mammalian matrix attachment regions (MARs) for increasing transcription and uses thereof for recombinant protein production, gene therapy or tissue replacement therapy
IN Mermod, Nicolas; Girod, Pierre Alain; Calabrese, David; Regamey, Alexandre; Doninelli-Arope, Saline
PA Selexis S.A., Switz.
SO PCT Int. Appl., 72 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2008023247	A2	20080228	WO 2007-IB2404	20070822
WO 2008023247	A3	20080508		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, SV, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW				
RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, LV, MC, MT, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AP, EA, EP, OA				
AU 2007287327	A1	20080228	AU 2007-287327	20070822
CA 2658775	A1	20080228	CA 2007-2658775	20070822
EP 2061883	A2	20090527	EP 2007-804795	20070822
R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LI, LT, LU, LV, MC, MT, NL, PL, PT, RO, SE, SI, SK, TR,				

AL, BA, HR, MK, RS
KR 2009053893 A 20090528 KR 2009-701885
20090129
CN 101541959 A 20090923 CN 2007-80029732
20090210
PRAI US 2006-823319P P 20060823
US 2007-953910P P 20070803
WO 2007-IB2404 W 20070822
AB Isolated and purified matrix attachment regions (MAR) sequences of human and non-human animal origin are disclosed as are nucleotide sequences corresponding to or based on them. In particular, MARs and MAR constructs with high transcription and/or protein production enhancing activities are disclosed and so are methods for identifying such MARs, designing such MAR constructs and employing them, e.g., for high yield production of proteins. Speifically provided are sequences for genetic constructs containing human MAR 1_68 and mouse MAR-S4. The invention provides for the use of the bioinformatics tool SMARScan in identifying human MARs. The invention also provides a multiple transfection method using vectors comprising said human MARs. In the examples, the invention demonstrated the use of MARs in increased production of enhanced green fluorescent proteins and mouse erythropoietin.

L11 ANSWER 21 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:395461 CAPLUS
DN 142:442890
TI Human matrix attachment regions (MARs), their sequences, identification using SMARScan and use in increased production of recombinant proteins in transfected eukaryotic cells
IN Mermod, Nicolas; Girod, Pierre Alain; Bucher, Philipp; Nguyen, Duc-Quang; Calabrese, David; Saugy, Damien; Puttini, Stefania
PA Selexis S.A., Switz.
SO PCT Int. Appl., 282 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1
PATENT NO. KIND DATE APPLICATION NO. DATE
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PI WO 2005040377 A2 20050506 WO 2004-EP11974
20041022
WO 2005040377 A3 20050915
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ,
CA, CH,
CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI,
GB, GD,
GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR,
KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NA, NI,
NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK,
SL, SY,
TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA,
ZM, ZW
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM,
ZW, AM,
AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ,
DE, DK,
EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT,
RO, SE,
SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML,
MR, NE,
SN, TD, TG
AU 2004284220 A1 20050506 AU 2004-284220
20041022
CA 2535836 A1 20050506 CA 2004-2535836
20041022
EP 1675952 A2 20060705 EP 2004-790766
20041022
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE,
MC, PT,
IE, SI, LT, LV, FI, RO, CY, TR, BG, CZ, EE, HU, PL, SK
CN 1863913 A 20061115 CN 2004-80029260
20041022
JP 2007508831 T 20070412 JP 2006-536060
20041022
EP 1959011 A2 20080820 EP 2008-153753
20041022
EP 1959011 A3 20080827
R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR,
HU, IE,
IT, LI, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, LT, LV
SG 147468 A1 20081128 SG 2008-7906
20041022
US 20070178469 A1 20070802 US 2006-595495
20060424
ZA 2006004032 A 20080528 ZA 2006-4032
20060519
PRAI US 2003-513574P P 20031024
EP 2004-2722 A 20040206
EP 2004-790766 A3 20041022

WO 2004-EP11974 W 20041022
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The invention provides isolated and purified DNA sequences composed of at least one bent DNA element and at least one binding site for a protein that has protein production increasing activity. Specifically, the invention provides DNA sequences for human matrix attachment regions (MARs), and provides a list of transcription factors that bind to said human MARs. More specifically, the invention provides the DNA sequences of MARs from human chromosomes 1 and 2, and MARs identified in human RefSeq sequences. The invention also provides for the use of the bioinformatics tool SMARScanin identifying said human S/MARs. The invention further provides for the use of said human MARs in increasing protein production activity in twice transfected eukaryotic host cells. Finally, the invention provides a new multiple transfection method using vectors comprising said human MARs. In the examples, the invention demonstrated the use of MARs in increased production of enhanced green fluorescent proteins and mouse erythropoietin.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 22 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:60897 CAPLUS
DN 143:299916
TI Screening, cloning, and sequence analysis of random MARS in the genome of human T cells
AU Mao, Qiongguo; Bai, Yun; Zhang, Bo; Huang, Gang; Wang, Yan; Dai, Jiaping
CS College of Medicine, Third Military Medical University, Chongqing, 400038, Peop. Rep. China
SO Di-San Junyi Daxue Xuebao (2004), 26(15), 1342-1345
CODEN: DYXUE8; ISSN: 1000-5404
PB Di-San Junyi Daxue Xuebao Bianjibu
DT Journal
LA Chinese
AB Objective: to screen and clone the fragment of random matrix association regions (MARs) in human genome and analyze the characteristics of their

sequences in order to provide the proof for further investigation of the mol. mechanisms of MARs in the regulation of eukaryotes gene expression. Methods: the fragment of the random MARs of human genome, isolated by treatment of the nuclei using DNase I, high salt, and protein K, was cloned into the PUC19 vector. MARs which could bind with nuclear matrix proteins were identified by binding assay in vitro and sequenced consequently. The characteristics were analyzed by the bioinformatic method. Results: a large number of MARs fragments were screened and obtained from human T cells successfully. An MARs library was constructed and 58 clones were selected randomly from the library. The results of the binding assay in vitro showed that the random MARs had binding activity with nuclear matrix proteins, and sequence anal. of one of the clones showed that it consisted of rich A and T base pairs, AC-rich elements and ATAT motifs, many origin points of transcription/replication, enhancer, curved DNA, kinked DNA regions, and numerous reverse repeated base sequences. Conclusion: the obtained DNA fragments have the characteristics of MARs and multiple cis-function elements in a DNA sequence, suggesting that the functions of MARs in regulation of gene expression are complicated and multiform.

L11 ANSWER 23 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2003:570688 CAPLUS
DN 139:112745
TI Use of avian lysozyme promoter for transgenic human interferon α2b and monoclonal antibody synthesis in oviduct cells
IN Rapp, Jeffrey C.
PA Avigenics, Inc., USA
SO U.S. Pat. Appl. Publ., 87 pp., Cont.-in-part of U.S. Ser. No. 922,549.
CODEN: USXXCO
DT Patent
LA English
FAN.CNT 10

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

PI US 20030140363 A1 20030724 US 2002-114739
20020401
US 7199279 B2 20070403
US 20020199214 A1 20021226 US 2001-922549
20010803
US 7176300 B2 20070213
US 20070124829 A1 20070531 US 2007-699257
20070126
US 7541512 B2 20090602
PRAI US 2001-280004P P 20010330
US 2001-922549 A2 20010803
US 2002-351550P P 20020125
US 2002-114739 A2 20020401
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The present invention provides novel isolated nucleic acids comprising an
avian nucleic acid sequence encoding a lysozyme gene expression control
region. The isolated nucleic acid of the present invention is useful for
reducing the chromosomal positional effect of a transgene operably linked
to the lysozyme gene expression control region and transfected into a
recipient cell and allows expression of an operably linked heterologous
nucleic acid insert in a transfected avian cell such as, for example, an
oviduct cell. The isolated avian lysozyme of the present invention may be
operably linked with a selected nucleic acid insert encoding a polypeptide
desired to be expressed in a transfected cell. The recombinant DNA of the
present invention may further comprise a polyadenylation signal sequence
or a chicken lysozyme 3' domain.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 59 THERE ARE 59 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 24 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:778151 CAPLUS
DN 137:274098
TI Use of avian lysozyme promoter for transgenic human interferon α2b
and monoclonal antibody synthesis in oviduct cells
IN Rapp, Jeffrey C.
PA Avigenics, Inc., USA
SO PCT Int. Appl., 88 pp.
CODEN: PIXXD2

DT Patent
LA English
FAN.CNT 10

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002079447	A2	20021010	WO 2002-US9866	20020329
WO 2002079447	A9	20021121		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 20020199214	A1	20021226	US 2001-922549	20010803
US 7176300	B2	20070213		
AU 2002255995	A1	20021015	AU 2002-255995	20020329
EP 1478751	A2	20041124	EP 2002-725432	20020329
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
PRAI US 2001-280004P	P	20010330		
US 2001-922549	A	20010803		
US 2002-351550P	P	20020125		
WO 2002-US9866	W	20020329		

ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT

AB The present invention demonstrates the use of an avian lysozyme promoter in transgenic human interferon α2b (gene IFNMAGMAX) and monoclonal antibody synthesis in oviduct cells. The isolated nucleic acid of the present invention is useful for reducing the chromosomal positional effect of a transgene operably linked to the lysozyme gene expression control

region and transfected into a recipient cell and allows expression of an operably linked heterologous nucleic acid insert in a transfected avian cells such as, for example, an oviduct cell. The isolated avian lysozyme of the present invention may be operably linked with a selected nucleic acid insert encoding a polypeptide desired to be expressed in a transfected cell. The recombinant DNA of the present invention may further comprise a polyadenylation signal sequence or a chicken lysozyme 3' domain.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L11 ANSWER 25 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:574287 CAPLUS
DN 137:289445
TI Global regulation of virulence determinants in Staphylococcus aureus by the SarA protein family
AU Cheung, Ambrose L.; Zhang, Gongyi
CS Department of Microbiology and Immunology, Dartmouth Medical School, Hannover, NH, 03755, USA
SO Frontiers in Bioscience [online computer file] (2002), 7, D1825-D1842
CODEN: FRBIF6; ISSN: 1093-4715
URL: http://www.bioscience.org/2002/v7/d/cheung/pdf.pdf
PB Frontiers in Bioscience
DT Journal; General Review; (online computer file)
LA English
AB A review. In S. aureus, the production of virulence determinants such as cell wall adhesins and exotoxins during the growth cycle is controlled by global regulators such as SarA and agr. Genomic scan reveals 16 two-component regulatory systems (e.g. agr and sae) as well as a family of SarA homologs in S. aureus. We call the SarA homologs the SarA protein family. Many of the members in this protein family are either small basic proteins (<153 residues) or two-domain proteins in which a single domain shares sequence similarity to each of the small basic proteins. Recent crystal structures of SarR and SarA reveal dimeric structures for these proteins. Because of its structure and unique mode of DNA binding, SarR,

and possibly other SarA family members, may belong to a new functional class of the winged-helix family, accommodating long stretch of DNA with bending points. AgrA. Based on sequence homol., we hypothesize that the SarA protein family may entail homologous structures with similar DNA-binding motifs but divergent activation domains. An understanding of how these regulators interact with each other in vivo and how they sense environmental signals to control virulence gene expression (e.g. α-hemolysin) will be important to our eventual goal of disrupting the regulatory network.
OSC.G 30 THERE ARE 30 CAPLUS RECORDS THAT CITE THIS RECORD (30 CITINGS)

L11 ANSWER 26 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:481730 CAPLUS
DN 137:242883
TI Characterization of the region encompassing the human lysyl oxidase locus
AU Martins, Rui Pires; Ujfalusi, Aniko A.; Csiszar, Katalin; Krawetz, Stephen A.
CS Center for Molecular Medicine and Genetics, Wayne State University School of Medicine, Detroit, MI, 48201, USA
SO DNA Sequence (2001), 12(4), 215-227
CODEN: DNSEES; ISSN: 1042-5179
PB Harwood Academic Publishers
DT Journal
LA English
AB A 46,823 bp region of human chromosome 5q23.1 encompassing the seven-exon lysyl oxidase gene was characterized at the primary sequence level. Approx. 17.4% of this region is comprised of repetitive elements. The gene colocalizes with microsatellite marker D5S467. It is flanked by two candidate nuclear matrix association regions (MARs). The 5' MAR centered at position 12,500 is of the AT-rich and curved DNA class. This is followed by a large CpG island containing fifty-seven putative regulatory elements which extend from just upstream of exon 1 to intron 2. The larger 3' MAR, spans position 35,050-39,750 and is characterized by a TG-rich kinked structure that also contains a topoisomerase II binding site. Based on these results model of the transcriptional regulation of the lysyl oxidase gene is

presented.
RE.CNT 66 THERE ARE 66 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 27 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2000:592058 CAPLUS
DN 134:52163
TI Analysis of genetic elements controlling Staphylococcus aureus lrgAB
expression: potential role of DNA topology in SarA regulation
AU Fujimoto, David F.; Brunskill, Eric W.; Bayles, Kenneth W.
CS Department of Microbiology, Molecular Biology and Biochemistry, University
of Idaho, Moscow, ID, 83844-3052, USA
SO Journal of Bacteriology (2000), 182(17), 4822-4828
CODEN: JOBAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
AB Penicillin-induced killing and murein hydrolase activity in Staphylococcus
aureus are dependent on a variety of regulatory elements, including the
LytSR two-component regulatory system and the virulence factor regulators
Agr and Sar. The LytSR effects on these processes can be
explained, in part, by the recent finding that a LytSR-regulated operon,
designated lrgAB, affects murein hydrolase activity and penicillin
tolerance. To examine the regulation of lrgAB expression in greater
detail, we performed Northern blot and promoter fusion analyses. Both
methods revealed that Agr and Sar, like LytSR, pos. regulate
lrgAB expression. A mutation in the agr locus reduced lrgAB expression
approx. sixfold, while the sar mutation reduced lrgAB expression
to undetectable levels. Cis-acting regulatory elements involved in lrgAB
expression were identified by fusing various fragments of the lrgAB
promoter region to the xylE reporter gene and integrating these constructs
into the chromosome. Catechol 2,3-dioxygenase assays identified DNA
sequences, including an inverted repeat and intrinsic bend sites, that
contribute to maximal lrgAB expression. Confirmation of the importance of
the inverted repeat was achieved by demonstrating that multiple copies of

the inverted repeat reduced lrgAB promoter activity, presumably by titrating out a pos. regulatory factor. The results of this study demonstrate that lrgAB expression responds to a variety of pos. regulatory factors and suggest that specific DNA topol. requirements are important for optimal expression.

OSC.G 21 THERE ARE 21 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)

RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 28 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN

AN 1997:448840 CAPLUS

DN 127:145805

OREF 127:28049a,28052a

TI The DNA sequence and structural characteristics of the 5'-nontranscribed spacer of silkworm Attacus ricini rDNA

AU He, Mingliang; Zhao, Mujun; Jin, Jiarui; Li, Zaioping

CS Shanghai Inst. Biochemistry, Acad. Sinica, Shanghai, 200031, Peop. Rep. China

SO Shengwu Huaxue Yu Shengwu Wuli Xuebao (1996), 28(6), 616-623
CODEN: SHWPAU; ISSN: 0582-9879

PB Shanghai Kexue Jishu Chubanshe

DT Journal

LA Chinese

AB The SacII-EcoRI fragment in the nontranscribed spacer (NTS) of silkworm Attacus ricini rDNA is a nuclear scaffold-associated region (SAR) and showed the function as the ARS element in yeast. The sequence of this NTS region and the various characteristic potential functional motifs were analyzed by computer. It is 1025 bp long and AT-rich, with 9 bent DNA motifs, 10 T-boxes, 5 A-boxes motifs, 13 topoisomerase II and 15 ARS consensus sequences. In addition, there are dozens of inferred repeats and ATTA/TAAT, ATTTA/TAAAT, ATATTT/AAATAT motifs commonly believed to be the binding sites of many homeodomain proteins. These motifs, concentrated in the SAR region, may play very important role in the regulation of gene transcription and replication at the chromatin level.

L11 ANSWER 29 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN

AN 1997:260799 CAPLUS
DN 126:326429
OREF 126:63319a,63322a
TI Mathematical model to predict regions of chromatin attachment to the nuclear matrix
AU Singh, Gautam B.; Kramer, Jeffrey A.; Krawetz, Stephen A.
CS Bioinformatics Algorithms Res. Div., Natl. Cent. Genome Resources, Santa Fe, NM, 87505, USA
SO Nucleic Acids Research (1997), 25(7), 1419-1425
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
AB The potentiation and subsequent initiation of transcription are complex biol. phenomena. The region of attachment of the chromatin fiber to the nuclear matrix, known as the matrix attachment region or scaffold attachment region (MAR or SAR), are thought to be requisite for the transcriptional regulation of the eukaryotic genome. As expressed sequences should be contained in these regions, it becomes significant to answer the following question: can these regions be identified from the primary sequence data alone and subsequently used as markers for expressed sequences This paper represents an effort toward achieving this goal and describes a math. model for the detection of MARs. The location of matrix associated regions has been linked to a variety of sequence patterns. Consequently, a list of these patterns is compiled and represented as a set of decision rules using an AND-OR formulation. The DNA sequence was then searched for the presence of these patterns and statistical significance was associated with the frequency of occurrence of the various patterns. Subsequently, a math. potential value, MAR-Potential, was assigned to a sequence region as the inverse proportion to the probability that the observed pattern population occurred at random. Such a MAR detection process was applied to the anal. of a variety of known MAR containing sequences. Regions of matrix association predicted by the software essentially correspond to those determined exptl. The human

T-cell receptor and the DNA sequence from the Drosophila bithorax region were also analyzed. This demonstrates the usefulness of the approach described as a means to direct exptl. resources.
OSC.G 140 THERE ARE 140 CAPLUS RECORDS THAT CITE THIS RECORD (140 CITINGS)

L11 ANSWER 30 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1996:206109 CAPLUS
DN 124:252034
OREF 124:46485a,46488a
TI Chromatin domains and prediction of MAR sequences
AU Boulikas, Teni
CS Institute Molecular Medical Sciences, Palo Alto, CA, 94306, USA
SO International Review of Cytology (1995), 162A(Structural and Functional Organization of the Nuclear Matrix), 279-388
CODEN: IRCYAJ; ISSN: 0074-7696
PB Academic
DT Journal
LA English
AB Polynucleosomes are constrained into loops or domains and are insulated from the effects of chromatin structure and torsional strain from flanking domains by the cross-complexation of matrix-attached regions (MARs) and matrix proteins. MARs or SARs have an average size of 500 bp, are spaced about every 30 kb, and are control elements maintaining independent realms of gene activity. A fraction of MARs may cohabit with core origins of replication (ORIs) and another fraction might cohabit with transcriptional enhancers. DNA replication, transcription, repair, splicing, and recombination seem to take place on the nuclear matrix. Classical AT-rich MARs have been proposed to anchor the core enhancers and core origins complexed with low abundance transcription factors to the nuclear matrix via the cooperative binding to MARs of abundant classical matrix proteins (topoisomerase II, histone H1, lamins, SP120, ARBP, SATB1); this creates a unique nuclear microenvironment rich in regulatory proteins able to sustain transcription, replication, repair, and recombination. Theor. searches and exptl. data strongly support a model of activation of MARs and ORIs by transcription factors. A set of 21 characteristics are deduced or proposed for MAR/ORI sequences including their

enrichment in inverted repeats, AT tracts, DNA unwinding elements, replication initiator protein sites, homo-oligonucleotide repeats (i.e., AAA, TTT, CCC), curved DNA, DNase I-hypersensitive sites, nucleosome-free stretches, polypurine stretches, and motifs with a potential for left-handed and triplex structures. We are establishing Banks of ORI and MAR sequences and have undertaken a large project of sequencing a large number of MARs in an effort to determine classes of DNA sequences in these regulatory elements and to understand their role at the origins of replication and transcriptional enhancers.
OSC.G 168 THERE ARE 168 CAPLUS RECORDS THAT CITE THIS RECORD (168 CITINGS)

L11 ANSWER 31 OF 31 EMBASE COPYRIGHT (c) 2009 Elsevier B.V. All rights reserved on STN
AN 2009095018 EMBASE
TI Open access article nucleosome DNA bendability matrix (C. elegans).
AU Gabdank, I. (correspondence); Barash, D.
CS Department of Computer Science Ben Gurion, University of the Negev, P.O.B 653 Be'er Sheva 84105, Israel.
AU Trifonov, E.N.
CS Genome Diversity Center, Institute of Evolution, University of Haifa Mount Carmel, Haifa 31905, Israel. trifonov@research.haifa.ac.il
AU Trifonov, E.N.
CS Division of Functional Genomics and Proteomics, Faculty of Science Masaryk University, Kamenice 5, Brno CZ-62500, Czech Republic. trifonov@research.haifa.ac.il
SO Journal of Biomolecular Structure and Dynamics, (February 2009) Vol. 26, No. 4, pp. 403-412.
Refs: 21
ISSN: 0739-1102 CODEN: JBSDD6
PB Adenine Press, 2066 Central Avenue, Schenectady, NY 12304, United States.
CY United States
DT Journal; Article
FS 004 Microbiology: Bacteriology, Mycology, Parasitology and Virology
021 Developmental Biology and Teratology
022 Human Genetics
LA English

SL English
ED Entered STN: 13 Mar 2009
Last Updated on STN: 13 Mar 2009
AB An original signal extraction procedure is applied to database of 146 base
nucleosome core DNA sequences from C. elegans (S. M. Johnson et al.
Genome Research 16, 1505-1516, 2006). The positional preferences of
various dinucleotides within the 10.4 base nucleosome DNA repeat are
calculated, resulting in derivation of the nucleosome DNA
bendability matrix of 16x10 elements. A simplified one-line
presentation of the matrix (" consensus" repeat) is (midline ellipsis)
A(TTTCCGGAAA)T (midline ellipsis). All 6 chromosomes of C. elegans
conform to the bendability pattern. The strongest affinity to their
respective positions is displayed by dinucleotides AT and CG, separated
within the repeat by 5 bases. The derived pattern makes a basis for
sequence-directed mapping of nucleosome positions in the genome of C.
elegans. As the first complete matrix of bendability available the
pattern may serve for iterative calculations of the species-specific
matrices of bendability applicable to other genomic sequences.

=> FIL STNGUIDE

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	107.75	209.33

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-9.02	-9.84

FILE 'STNGUIDE' ENTERED AT 17:21:22 ON 21 OCT 2009

FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Oct 16, 2009 (20091016/UP).

=> FIL BIOSIS CAPLUS EMBASE

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=>
COST IN U.S. DOLLARS                                    SINCE FILE      TOTAL
                                                           ENTRY    SESSION
FULL ESTIMATED COST                                         3.78     213.11

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)              SINCE FILE      TOTAL
                                                           ENTRY    SESSION
CA SUBSCRIBER PRICE                                         0.00
-9.84

FILE 'BIOSIS' ENTERED AT 17:53:45 ON 21 OCT 2009
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=> d his

     (FILE 'HOME' ENTERED AT 16:13:54 ON 21 OCT 2009)

     FILE 'BIOSIS, CAPLUS, EMBASE' ENTERED AT 16:22:59 ON 21 OCT 2009
L1         11123 S (BEND? OR BENT OR CURV?) (3A) DNA
L2         64211 S MATRIX ATTACHMENT REGION OR SCAFFOLD ATTACHMENT
REGION OR MAR
L3           108 S L1 AND L2
L4             0 S L3 AND GROOVE AND MELTING TEMPERATURE
L5             0 S L1 AND MAJOR GROOVE AND MINOR GROOVE AND MELTING
TEMPERATURE
L6            71 S L1 AND MELTING TEMPERATURE
L7             3 S L6 AND GROOVE
L8             2 DUP REM L7 (1 DUPLICATE REMOVED)
L9            56 DUP REM L3 (52 DUPLICATES REMOVED)
L10            2 S L9 AND REVIEW

     FILE 'STNGUIDE' ENTERED AT 16:36:48 ON 21 OCT 2009

     FILE 'BIOSIS, CAPLUS, EMBASE' ENTERED AT 17:08:41 ON 21 OCT 2009
L11           31 S L9 AND TRANSCRIPT?

     FILE 'STNGUIDE' ENTERED AT 17:21:22 ON 21 OCT 2009

     FILE 'BIOSIS, CAPLUS, EMBASE' ENTERED AT 17:53:45 ON 21 OCT 2009

=> s lysozyme (3a) l2
L12          64 LYSOZYME (3A) L2
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=> s l12 and (chicken or avian)
L13         60 L12 AND (CHICKEN OR AVIAN)

=> dup rem l13
PROCESSING COMPLETED FOR L13
L14          31 DUP REM L13 (29 DUPLICATES REMOVED)

=> d bib abs 1-
YOU HAVE REQUESTED DATA FROM 31 ANSWERS - CONTINUE? Y/(N):y

L14  ANSWER 1 OF 31  BIOSIS  COPYRIGHT (c) 2009 The Thomson
Corporation  on STN
AN   2008:159475  BIOSIS
DN   PREV200800169083
TI   Influence of a matrix attachment region on the expression of
bicistronic
     vectors transfected in mammalian cells cultured In vitro.
AU   Perota, A. [Reprint Author]; Brunetti, D.; Lizier, M.; Lucchini,
F.;
     Galli, C.
CS   LTR, CIZ, I-26100 Cremona, Italy
SO   Reproduction Fertility and Development, (2008) Vol. 20, No. 1,
pp. 234.
     Meeting Info.: Annual Conference of the
     International-Embryo-Transfer-Society. Denver, CO, USA. January
05 -09,
     2008. Int Embryo Transfer Soc.
     ISSN: 1031-3613.
DT   Conference; (Meeting)
     Conference; (Meeting Poster)
LA   English
ED   Entered STN: 5 Mar 2008
     Last Updated on STN: 5 Mar 2008

L14  ANSWER 2 OF 31  CAPLUS  COPYRIGHT 2009 ACS on STN
AN   2007:201378  CAPLUS
DN   146:250320
TI   Production of a therapeutic antibody comprising the use of
chicken
     insulator elements flanking the Ig sequence
IN   Singh, Sanjaya
PA   Tanox, Inc., USA
SO   PCT Int. Appl., 27pp.
     CODEN: PIXXD2
DT   Patent
LA   English
FAN.CNT 1
     PATENT NO.          KIND   DATE        APPLICATION NO.
DATE
     ---------------     ----   --------    --------------------
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PI   WO 2007021353        A2    20070222    WO 2006-US22131
20060607
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WO 2007021353 A3 20070830
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH,
CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD,
GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR,
KZ, LC, LK, LR, LS, LT, LU, LV, LY, MA, MD, MG, MK, MN, MW, MX,
MZ, NA, NG, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RS, RU, SC, SD,
SE, SG, SK, SL, SM, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ,
VC, VN, ZA, ZM, ZW
RW: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE,
IS, IT, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ,
CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG, BW, GH,
GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY,
KG, KZ, MD, RU, TJ, TM, AP, EA, EP, OA
AU 2006280428 A1 20070222 AU 2006-280428 20060607
CA 2611465 A1 20070222 CA 2006-2611465 20060607
EP 1899478 A2 20080319 EP 2006-813200 20060607
R: AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE,
IS, IT, LI, LT, LU, LV, MC, NL, PL, PT, RO, SE, SI, SK, TR, AL,
BA, HR, MK, YU
JP 2008543283 T 20081204 JP 2008-515874 20060607
MX 2007015540 A 20080307 MX 2007-15540 20071207
PRAI US 2005-689623P P 20050610
WO 2006-US22131 W 20060607
AB The present invention relates to the improved production of a therapeutic
antibody comprising the use of insulator elements flanking the Ig sequence. The nucleotide sequence of chicken insulator element has been presented. Cell survival is also improved with the increase in
the number of insulator elements.

L14 ANSWER 3 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2007:487678 CAPLUS
DN 147:500856
TI The role of matrix-attachment regions in increasing recombinant protein

expression
AU Fisch, Igor
CS Selexis, Plan-les-Ouates, 1228, Switz.
SO BioProcess International (2007), 5(2), 66, 68, 70-73
CODEN: BIINCE; ISSN: 1542-6319
PB Informa Life Sciences Group
DT Journal; General Review
LA English
AB A review. Matrix-attachment region (MAR) elements influence gene expression by anchoring active chromatin domains to the nuclear matrix. When a flanking transgene is introduced into mammalian cells, MARs enhance the transgene expression. Naturally occurring MARs have a number of sequence features and DNA elements in common. By using different subsets of those sequence elements, a synthetic MAR is created, that bound nuclear scaffold prepns. with an affinity greater than the naturally occurring chicken lysozyme MAR. The synthetic MAR element from Selexis shows that >60% of the transgene is associated with a high transcription region. When these elements have been used to produce a secreted protein, such as an antibody, production levels exceed 80/p/c/d. Selexis has created more than 30 GLP-documented cell lines that produce recombinant proteins at levels ranging on average from 40 p/c/d to more than 100 p/c/d, all in a matter of weeks from transfection. They have established cell lines in baby hamster kidney cells, human embryonic 293 cells (HEK293), a B cell line, and the mouse cell line C2C12. The technol. works with both viral promoters and cellular promoters, including cytomegalovirus (CMV), simian virus 40, the ubiquitin promoter, and elF alpha.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 4 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:523642 CAPLUS
DN 143:54509
TI Post-transcriptional gene silencing suppression of matrix attachment region element-flanked target genes in transgenic Arabidopsis results in

enhanced expression of β-glucuronidase
IN Cammue, Bruno Philippe Angelo; De Bolle, Miguel Francesco Coleta; Butaye, Katleen
PA Plant Bioscience Limited, UK
SO PCT Int. Appl., 51 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2005054483	A2	20050616	WO 2004-GB5058	20041130
WO 2005054483	A3	20070222		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
AU 2004294508	A1	20050616	AU 2004-294508	20041130
CA 2545687	A1	20050616	CA 2004-2545687	20041130
EP 1706496	A2	20061004	EP 2004-819725	20041130
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, PL, SK, HR, IS, YU				
US 20080092252	A1	20080417	US 2006-581472	20061102
PRAI GB 2003-27919	A	20031202		

WO 2004-GB5058 W 20041130
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB Disclosed herein are methods and means of achieving enhanced expression of a target nucleotide sequence in a transgenic organism, which methods comprise the steps of; (i) providing an organism in which post-transcriptional gene silencing (PTGS) is suppressed, (ii) associating said target nucleotide sequence with one or more heterologous Matrix Attachment Region (MARs), and (iii) causing or permitting expression from the target nucleotide sequence in the organism. Plasmids with or without the chicken lysozyme MAR element were constructed, containing the uidA gene under the control of the 35S cauliflower mosaic virus promoter. Following genetic transformation into Arabidopsis thaliana, under normal or mutant conditions (mutant gene sgs2 or sgs3), the role of the MAR in post-transcriptional gene silencing of the target gene (uidA) was assayed by β-glucuronidase expression in leaf exts. Unexpectedly, the MARs do not merely relieve gene silencing, but can actually lead to expression levels higher than can be achieved in wild-type organisms and higher than expression levels in organisms in which PTGS is suppressed but where the MARs are not employed.
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 5 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 1
AN 2005:213483 BIOSIS
DN PREV200510007822
TI Expression of Escherichia coli branching enzyme in caryopses of transgenic rice results in amylopectin with an increased degree of branching.
AU Kim, Won-Seok; Kim, Jukon; Krishnan, Hari B.; Nahm, Baek Hie [Reprint Author]
CS Myongji Univ, Dept Biosci and Bioinformat, Yongin 449728, South Korea
bhnahm@mju.ac.kr
SO Planta (Berlin), (MAR 2005) Vol. 220, No. 5, pp. 689-695.
CODEN: PLANAB. ISSN: 0032-0935.

DT Article
LA English
ED Entered STN: 10 Jun 2005
Last Updated on STN: 10 Jun 2005
AB Physiochemical properties of starch are dependent on several factors including the relative abundance of amylose and amylopectin, and the degree of branching of amylopectin. Utilizing Agrobacterium-mediated transformation, a construct containing the coding region of branching enzyme of Escherichia coli, under transcriptional control of the rice (Oryza sativa L.) starch-branching enzyme promoter was introduced into rice cv. Nakdong. To enhance glgB expression, the first intron of rice starch-branching enzyme and the matrix attachment region (MAR) sequence from chicken lysozyme were included in the expression vector. Eleven independent transgenic rice plants were generated. Southern blot analysis indicated that the copy number of glgB integrated into transgenic rice varied from one to five. High-performance liquid chromatographic analysis of starch from transgenic lines revealed that amylopectin from transgenic lines exhibited greater branching than that of non-transgenic rice. The A/B1 ratio in amylopectin increased from 1.3 to 2.3 and the total branching ratio, A+B1/B-rest, increased from 6 to 12 in transgenic rice. The observed increase in the short-chain fractions with a degree of polymerization between 6 and 10 is expected to have a significant effect on retrogradation. Our study demonstrates that amylopectin branching can be altered in vivo, thus changing the physicochemical properties of starch.

L14 ANSWER 6 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:1029690 CAPLUS
DN 144:252730
TI MAR elements as tools to increase protein production by CHO cells
AU Girod, P.-A.; Zahn-Zabal, M. M.; Mermod, N.
CS Laboratory of Molecular Biotechnology, FSB-ISP, EPFL, University of Lausanne CBUE, Lausanne, 1015, Switz.
SO Animal Cell Technology Meets Genomics, Proceedings of the ESACT Meeting,

18th, Granada, Spain, May 11-14, 2003 (2005), Meeting Date 2003, 411-415.
Editor(s): Godia, Francesc; Fussenegger, Martin. Publisher: Springer,
Dordrecht, Neth.
CODEN: 69HJAV; ISBN: 1-4020-2791-5
DT Conference
LA English
AB One of the major hurdles of isolating stable, inducible or constitutive high-level producer cell lines is the time-consuming selection, anal. and characterization of the numerous clones required to identify one with the desired characteristics. Various boundary elements, matrix attachment regions, and locus control regions were screened for their ability to augment the expression of heterologous genes in CHO and other cells. The 5'-matrix-attachment region (MAR) of the chicken lysozyme gene was found to significantly increase stable gene expression, in culture dishes and in bioreactors. These MAR elements can be easily combined with various existing expression systems, as they can be added in trans (i.e. on a sep. plasmid) in co-transfections with previously constructed expression vectors. Using cell population anal., we found that the use of the MAR increases the proportion of high-producing CHO cell clones, thus reducing the number of cell lines that need to be screened while increasing maximal productivity. Random cDNA cloning and sequencing indicated that over 12% of the ESTs correspond to the transgene. Thus, productivity is no longer limited by transcriptional events in such MAR-containing cell lines. The identification of small and more convenient active MAR portions will also be summarized. Finally, we will show examples of how MAR elements can be combined with short term expression to increase the simultaneous synthesis of many proteins in parallel by CHO cells. Overall, we conclude that the MAR sequence is a versatile tool to increase protein expression in short and long term production processes.

OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 7 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 2
AN 2005:350572 BIOSIS
DN PREV200510142866
TI Matrix attachment region from the
chicken lysozyme locus reduces variability in transgene
expression and confers copy number-dependence in transgenic rice plants.
AU Oh, S.-J.; Jeong, J. S.; Kim, E.-H.; Yi, N. R.; Yi, S.-I.; Jang, I.-C.;
Kim, Y. S.; Suh, S.-C.; Nahm, B. H.; Kim, J.-K. [Reprint Author]
CS Myongji Univ, Div Biosci and Bioinformat, Yongin 449728, South Korea
jukon@mju.ac.kr
SO Plant Cell Reports, (JUN 2005) Vol. 24, No. 3, pp. 145-154.
CODEN: PCRPD8. ISSN: 0721-7714.
DT Article
LA English
ED Entered STN: 8 Sep 2005
Last Updated on STN: 8 Sep 2005
AB Matrix-attachment regions (MARs) may function as domain boundaries and
partition chromosomes into independently regulated units. In this study,
BP-MAR, a 1.3-kb upstream fragment of the 5' MAR flanking the
chicken lysozyme locus, was tested for its effects on
integration and expression of transgenes in transgenic rice plants. Using
the Agrobacterium-mediated method, we transformed rice with nine different
constructs containing seven and six different promoters and coding
sequences, respectively. Genomic Southern blot analyses of 357
independent transgenic lines revealed that in the presence of BP-MAR, 57%
of the lines contained a single copy of the transgene, whereas in its
absence, only 20% of the lines contained a single copy of the transgene.
RNA gel-blot and immunoblot experiments demonstrated that in the presence
of BP-MAR, transgene expression levels were similar among different lines.
These data were in direct contrast to those derived from transgenes
expressed in the absence of BP-MAR, which varied markedly with the

chromosomal integration site . Thus, it can be concluded that BP-MAR significantly reduces the variability in transgene expression between independent transformants. Moreover, the presence of BP-MAR appears to confer a copy number-dependent increase in transgene expression, although it does not increase expression levels of individual transgenes. These data contrast with results previously obtained with various MARs that increased expression levels of transgene significantly. Therefore, we conclude that the incorporation of BP-MAR sequences into the design of transformation vectors can minimize position effects and regulate transgene expression in a copy number-dependent way.

L14 ANSWER 8 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2005:1296659 CAPLUS
DN 145:21888
TI The effect of MAR elements from chicken lysozyme gene on the transient expression of β-glucuronidase reporter gene in soybean
AU Yang, Shaohui; Ding, Dongfeng; Hou, Jianhua; Ludmila, Mlynaova; Li, Minggang
CS Institute of Molecular Biology, Nankai University, Tianjin, 300071, Peop. Rep. China
SO Nankai Daxue Xuebao, Ziran Kexueban (2005), 38(4), 132-136
CODEN: NDXZAG; ISSN: 0465-7942
PB Nankai Daxue Xuebao Bianjibu
DT Journal
LA English
AB This paper presents a study on the influence of the chiMAR on the transient expression of β-glucuronidase (GUS) reporter gene (uidA) in soybean transformed with the vector pLM9 and vector pLM5. The results showed that the transient expression efficiency (TEE) of the uidA in soybean was observably boosted ($p<0.01$) by the chiMAR, but the influence on the transient expression levels (TELs) of the uidA between soybean variety Kefeng 6 and Jidou 12 was different. The TELs of the uidA were not markedly influenced but the transient expression variability (TEV) was markedly reduced by the chiMAR in Kefeng 6. However, the TELs and TEV of

the uidA were both markedly reduced in Jidou 12 by the chiMAR.
RE.CNT 12 THERE ARE 12 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 9 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN
DUPLICATE 3
AN 2005:391175 BIOSIS
DN PREV200510174349
TI Use of the chicken lysozyme 5 ' matrix attachment region to generate high producer CHO cell lines.
AU Girod, Pierre-Alain; Zahn-Zabal, Monique; Mermod, Nicolas [Reprint Author]
CS UNIL BEP, Ludwig Inst Canc Res, Off Informat Technol, CH-1015 Lausanne,
Switzerland
Nicolas.Mermod@unil.ch
SO Biotechnology and Bioengineering, (JUL 5 2005) Vol. 91, No. 1, pp. 1-11.
CODEN: BIBIAU. ISSN: 0006-3592.
DT Article
LA English
ED Entered STN: 28 Sep 2005
Last Updated on STN: 28 Sep 2005
AB Scaffold or matrix attachment region (S/MAR) genetic elements have previously been proposed to insulate transgenes from repressive effects linked to their site of integration within the host cell genome. We have evaluated their use in various stable transfection settings to increase the production of recombinant proteins such as monoclonal antibodies from Chinese hamster ovary (CHO) cell lines. Using the green fluorescent protein coding sequence, we show that S/MAR elements mediate a dual effect on the population of transfected cells. First, S/MAR elements almost fully abolish the occurrence of cell clones that express little transgene that may result from transgene integration in an unfavorable chromosomal environment. Second, they increase the overall expression of the transgene over the whole range of expression levels, allowing the detection of cells with significantly higher levels of transgene expression. An optimal setting was identified as the addition of a S/MAR element both in cis (on the transgene expression vector) and in trans

(co-transfected on a separate plasmid). When used to express immunoglobulins, the S/MAR element enabled cell clones with high and stable levels of expression to be isolated following the analysis of a few cell lines generated without transgene amplification procedures. (c) 2005 Wiley Periodicals, Inc.

L14 ANSWER 10 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 4

AN 2003:153615 BIOSIS
DN PREV200300153615
TI Optimization of cis-acting elements for gene expression from nonviral vectors in vivo.
AU Ehrhardt, Anja; Peng, Peter D.; Xu, Hui; Meuse, Leonard; Kay, Mark A.
[Reprint Author]
CS Departments of Pediatrics and Genetics, School of Medicine, Stanford University, 300 Pasteur Drive, Grant Building, Room G 305, Stanford, CA, 94305, USA
Markay@stanford.edu
SO Human Gene Therapy, (February 10 2003) Vol. 14, No. 3, pp. 215-225. print.
ISSN: 1043-0342 (ISSN print).
DT Article
LA English
ED Entered STN: 26 Mar 2003
Last Updated on STN: 26 Mar 2003
AB While naked DNA gene transfer in vivo usually results in transient gene expression, in some cases long-term transgene expression can be achieved. Here we demonstrate that cis-acting DNA elements flanking the transgene expression cassette and components in the plasmid backbone can significantly influence expression levels from nonviral vectors. To demonstrate this, we administered our most robust human coagulation factor IX (hFIX) expression cassette placed in two different plasmid backbones, into the livers of mice, by hydrodynamic transfection. We found that placing the expression cassette within a minimal plasmid vector pHM5, a modified version of pUC19, resulted in 10 times higher serum hFIX expression levels (up to 20,000 ng/ml, 400% of normal hFIX serum levels),

compared to a pBluescript backbone. To optimally increase expression levels from a nonviral vector, we added matrix attachment regions (MARs) as cis-acting DNA elements flanking the hFIX expression cassette. We detected five fold higher hFIX expression levels in vivo for up to 1-year posttransfection from a vector that contained the chicken MAR from the lysozyme locus. Together, the present work demonstrates that in addition to the transgene expression cassette, cis-acting DNA elements within and outside of the plasmid backbone need to be evaluated to achieve optimal expression levels in a nonviral gene therapy approach.

L14 ANSWER 11 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2002:736414 CAPLUS
DN 137:258470
TI Use of matrix attachment regions to improve transgene expression in eukaryotic cells
IN Mermod, Nicolas; Zahn-Zabal, Monique; Imhof, Markus; Chatellard, Philippe; Girod, Pierre-Alain
PA University of Lausanne, Switz.
SO PCT Int. Appl., 52 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002074969	A2	20020926	WO 2002-IB2137	20020128
WO 2002074969	A3	20031224		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY,

KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB,
GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA,
GN, GQ, GW, ML, MR, NE, SN, TD, TG
CA 2435972 A1 20020926 CA 2002-2435972 20020128
AU 2002256863 A1 20021003 AU 2002-256863 20020128
US 20030087342 A1 20030508 US 2002-59561 20020128
US 7129062 B2 20061031
EP 1395669 A2 20040310 EP 2002-726395 20020128
EP 1395669 B1 20090722
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO, MK, CY, AL, TR
JP 2004519246 T 20040702 JP 2002-574359 20020128
JP 4307079 B2 20090805
SG 141239 A1 20080428 SG 2005-4635 20020128
AT 437233 T 20090815 AT 2002-726395 20020128
PRAI US 2001-264355P P 20010126
US 2001-281391P P 20010404
WO 2002-IB2137 W 20020128
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB The present invention relates to compns. and method for transfecting eukaryotic cells with nucleic acid vectors. In particular, the invention relates to uses of MAR elements to increase stable and transient transfection efficiency. Thus, chicken lysozyme 5'-MAR element was able to significantly improve stable transgene expression in CHO cells. This MAR element also significantly improved transient transgene expression, particularly when the transfected cells were treatment with Na butyrate. Cotransfection of a plasmid containing the chicken lysozyme MAR element with one or more expression vectors also resulted in increased transgene expression.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)
RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 12 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2001:292556 CAPLUS

DN 135:353448
TI Expression of tPA directed by bovine beta-lactoglobulin (BLG) regulatory
element in mammary gland of transgenic mice
AU Chen, Hongxing; Cheng, Xuan; Yang, Xiao; Deng, Jixian; Su, Guofu; Huang,
Peitang
CS Institute of Biotechnology, The Academy of Military Medical Sciences,
Beijing, 100071, Peop. Rep. China
SO Shengwu Gongcheng Xuebao (2001), 17(2), 135-139
CODEN: SGXUED; ISSN: 1000-3061
PB Kexue Chubanshe
DT Journal
LA Chinese
AB The expression of tPA directed by bovine beta-lactoglobulin regulatory
element in mammary gland of transgenic mice was studied by PCR
amplification. The 1.6 kb chicken lysozyme
matrix attachment region (MAR) was
used to overcome position effect. The bovine BLG-tPA expression vector
was constructed and the BLG-tPA fusion gene was introduced into fertilized
eggs of mice by microinjection to generate transgenic mouse. Some 170
offsprings were obtained, of which 9 were proved to be transgenic mice
based on PCR and Southern-blot anal. The tPA expression level amounted to
12 μg/mL in the milk of mice. The bovine BLG-tPA fusion gene
integrated in the founders was inheritable.

L14 ANSWER 13 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN DUPLICATE 5
AN 2001:267262 BIOSIS
DN PREV200100267262
TI Development of stable cell lines for production or regulated expression
using matrix attachment regions.
AU Zahn-Zabal, Monique; Kobr, Michel; Girod, Pierre-Alain; Imhof, Markus;
Chatellard, Philippe; de Jesus, Maria; Wurm, Florian; Mermod, Nicolas
[Reprint author]
CS Laboratory of Molecular Biotechnology, Center for Biotechnology UNIL-EPFL,
CBUE, DC-IGC, University of Lausanne, CH-1015, Lausanne, Switzerland
nicolas.mermod@iba.unil.ch
SO Journal of Biotechnology, (27 April, 2001) Vol. 87, No. 1, pp. 29-42.

print.
CODEN: JBITD4. ISSN: 0168-1656.
DT Article
LA English
ED Entered STN: 6 Jun 2001
Last Updated on STN: 19 Feb 2002
AB One of the major hurdles of isolating stable, inducible or constitutive high-level producer cell lines is the time-consuming selection procedure. Given the variation in the expression levels of the same construct in individual clones, hundreds of clones must be isolated and tested to identify one or more with the desired characteristics. Various boundary elements (BEs), matrix attachment regions, and locus control regions(LCRs) were screened for their ability to augment the expression of heterologous genes in Chinese hamster ovary (CHO) cells. Of the chromatin elements assayed, the chicken lysozyme matrix-attachment region (MAR) was the only element to significantly increase stable reporter expression. We found that the use of the MAR increases the proportion of high-producing clones, thus reducing the number of clones that need to be screened. These benefits are observed both for constructs with MARs flanking the transgene expression cassette, as well as when constructs are co-transfected with the MAR on a separate plasmid. Moreover, the MAR was co-transfected with a multicomponent regulatable beta-galactosidase expression system in C2C12 cells and several clones exhibiting regulated expression were identified. Hence, MARs are useful in the development of stable cell lines for production or regulated expression.

L14 ANSWER 14 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 2000:881291 CAPLUS
DN 134:37901
TI Methods for the preparation of transgenic avian animals
IN Ditullio, Paul A.; Ebert, Karl M.
PA Tranxenogen, Inc., USA
SO PCT Int. Appl., 24 pp.
CODEN: PIXXD2
DT Patent

LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000075300	A2	20001214	WO 2000-US40059	20000602
WO 2000075300	A3	20020110		
W: AU, CA, JP, NZ, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
CA 2375441	A1	20001214	CA 2000-2375441	20000602
AU 2000057898	A	20001228	AU 2000-57898	20000602
AU 777420	B2	20041014		
EP 1190042	A2	20020327	EP 2000-943424	20000602
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2003501083	T	20030114	JP 2001-502566	20000602
NZ 516173	A	20040227	NZ 2000-516173	20000602
PRAI US 1999-137761P	P	19990604		
WO 2000-US40059	W	20000602		

AB The invention features a method for introducing a nucleic acid mol. into the genome of an avian species by contacting in vivo a blastodermal cell of a fertilized egg with the nucleic acid mol., which nucleic acid is not associated with a viral coat protein. The invention also encompasses transgenic avian animals and methods of producing such transgenic animals. The invention is exemplified by making transgenic chickens through microinjecting lactoferrin expression vectors which can express insulin genes from various species under the control of human lactoferrin gene promoter. These transgenic avian animals may also be applied for the production of tetrameric antibodies.

OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 15 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 6

AN 2000:159892 BIOSIS
DN PREV200000159892
TI Codon optimization, genetic insulation, and an rtTA reporter improve performance of the tetracycline switch.
AU Wells, Kevin D.; Foster, Juli A.; Moore, Karen; Pursel, Vernon G.; Wall, Robert J. [Reprint author]
CS Gene Evaluation and Mapping Laboratory, LPSI, BARC, USDA-ARS, BARC-East, Bldg. 200, RM 8, Beltsville, MD, 20705, USA
SO Transgenic Research, (Oct., 1999) Vol. 8, No. 5, pp. 371-381. print.
ISSN: 0962-8819.
DT Article
LA English
ED Entered STN: 26 Apr 2000
Last Updated on STN: 4 Jan 2002
AB The objective of this work was to further develop a tetracycline repressor (TetR) protein system that allows control of transgene expression. First, to circumvent the need for a binary approach, a single plasmid design was constructed and tested in tissue culture. To indirectly assay integrations that express the synthetic transcription factor (rtTA), a bicistronic gene was built which included an internal ribosome entry site (IRES) and a green fluorescent protein coding region (GFP) on the same expression cassette as the coding region of rtTA (pTetGREEN). This construct did not produce fluorescent colonies when stably integrated and provided minimal expression of GFP in the face of adequate expression of rtTA. The coding region for TetR was then altered by introducing 156 silent point mutations to simulate mammalian genes. Replacement of wild-type TetR gene (tetR) in pTetGREEN with 'mammalianized' tetR provided GFP expression. Adjustment of codon usage in the tetR region of rtTA nearly doubled the expression level of functional rtTA. To increase the number of rtTA expressing lines, the chicken egg-white lysozyme matrix attachment region (MAR) was introduced into the single plasmid design just upstream of the tetracycline operators (tetO). Inclusion of the MAR doubled the

number of colonies that expressed rtTA (44% vs 88%). With the modifications described here, the number of lines that express rtTA and provide induction from a single plasmid design can be increased by the inclusion of a MAR and the level of rtTA expression can be further increased by adjusting the base composition of the TetR coding region. The MAR also insulates the inducible gene from the promoter driving rtTA.

L14 ANSWER 16 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1998:251277 CAPLUS
DN 128:279566
OREF 128:55249a,55252a
TI Enhanced β-glucuronidase transgene expression in a population of monocot cells employing scaffold attachment regions of chicken lysozyme gene
IN Odell, Joan Tellefsen; Krebbers, Enno
PA E. I. Du Pont de Nemours & Co., USA
SO PCT Int. Appl., 28 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9816650	A1	19980423	WO 1997-US17709	19971001
W: AL, AM, AU, AZ, BA, BB, BG, BR, BY, CA, CN, CU, CZ, EE, GE, HU, ID, IL, IS, JP, KG, KP, KR, KZ, LC, LK, LR, LT, LV, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, SL, TJ, TM, TR, TT, UA, US, UZ, VN, YU				
RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
CA 2263891	A1	19980423	CA 1997-2263891	19971001
AU 9748933	A	19980511	AU 1997-48933	19971001
EP 931155	A1	19990728	EP 1997-911608	19971001
R: CH, DE, DK, ES, FR, GB, IT, LI, NL, SE				
BR 9712532	A	19991019	BR 1997-12532	19971001

JP 2000504943 T 20000425 JP 1998-518390
19971001
HU 2000000064 A2 20000528 HU 2000-64
19971001
HU 2000000064 A3 20020228
MX 9903284 A 20000228 MX 1999-3284
19990408
KR 2000049209 A 20000725 KR 1999-703308
19990416
PRAI US 1996-28165P P 19961017
WO 1997-US17709 W 19971001
AB A method of increasing transgene expression in a population of
monocot
plant cells is described which involves the use of a DNA
construct
comprising, inter alia, at least one chicken lysozyme
gene locus scaffold attachment region (SAR).
The method is exemplified by transformation of corn cells with
plasmid
vectors containing the above-mentioned SAR, a cauliflower mosaic
virus 35S
promoter, the β-glucuronidase gene uidA, and the nopaline
synthase
gene polyadenylation signal sequence.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4
CITINGS)
RE.CNT 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 17 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson
Corporation on
STN DUPLICATE 7
AN 1998:361965 BIOSIS
DN PREV199800361965
TI An initiation zone of chromosomal DNA replication at the chicken
lysozyme gene locus.
AU Phi-Van, Loc [Reprint author]; Sellke, Claudia; Von Bodenhausen,
Alexandra; Straetling, Wolf H.
CS Institut fuer Tierzucht und Tierverhalten, Doernbergstr. 25-27,
29223
Celle, Germany
SO Journal of Biological Chemistry, (July 17, 1998) Vol. 273, No.
29, pp.
18300-18307. print.
CODEN: JBCHA3. ISSN: 0021-9258.
DT Article
LA English
ED Entered STN: 27 Aug 1998
Last Updated on STN: 27 Aug 1998
AB The chicken lysozyme gene domain is distinguished by a broad
knowledge of how its expression is regulated. Here, we examined
the in

vivo replication of the lysozyme gene locus using polymerase chain reaction amplification and competitive polymerase chain reaction of size-fractionated, nascent DNA strands. We found that DNA replication initiates at multiple sites within a broad initiation zone spanning at least 20 kilobases, which includes most of the lysozyme gene domain. The 5' border of this zone is probably located downstream of the lysozyme 5' nuclear matrix attachment region. Preferred initiation occurs in a 3'-located subzone. The initiation zone at the lysozyme gene locus is also active in nonexpressing liver DU249 cells. Furthermore, examining the timing of DNA replication at the lysozyme gene locus revealed that the gene locus replicates early during S phase in both HD11 and DU249 cells, irrespective of its transcriptional activity.

L14 ANSWER 18 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1998:803088 CAPLUS
DN 130:178016
TI Matrix attachment region sequences enhanced the expression frequency of a whey acidic protein/human lactoferrin fusion gene in the mammary gland of transgenic mice
AU Lee, Tae-Hoon; Kim, Sun Jung; Han, Yong-Mahn; Yu, Dae-Yeul; Lee, Chul-Sang; Choi, Yun-Jaie; Moon, Hyung-Bae; Baik, Myung-Gi; Lee, Kyung-Kwang
CS Plant and Animal Cell Technology Research Division, Korea Research Institute of Bioscience and Biotechnology, Taejon, 305-333, S. Korea
SO Molecules and Cells (1998), 8(5), 530-536
CODEN: MOCEEK; ISSN: 1016-8478
PB Springer-Verlag Singapore Pte. Ltd.
DT Journal
LA English
AB To elevate the expression frequency of transgenes in transgenic mice, the chicken lysozyme matrix attachment region (MAR) sequence was used by combining it with a transgene. The whey acidic protein (WAP) promoter/human lactoferrin (hLF) cDNA fusion transgene (pWL) was connected to the chicken lysozyme MAR sequence at its 5'-end (pMWL). While only two of three mice became transgenic from the pWL vector expressed hLF, all

seven mice from the pMWL vector expressed the transgene in their lactating mammary glands. To evaluate the effect of lactogenic hormones on transgene expression, expts. with the primary culture of transgenic mammary explants were performed. It was revealed that the expression of transgenes was slightly increased by insulin plus dexamethasone or insulin plus prolactin treatment. However it was not increased by insulin, dexamethasone or prolactin (IDP) treatment alone. In contrast, the endogenous WAP gene was expressed only in the IDP treated group. These results demonstrate that MAR sequences are effective in improving the expression frequency of transgenes in transgenic mice although the developmental and hormonal regulations are not the same as those of the endogenous WAP gene.

OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)

RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 19 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 8

AN 1997:438542 BIOSIS

DN PREV199799737745

TI Chicken MAR-binding protein ARBP is homologous to rat methyl-CpG-binding protein MeCP2.

AU Weitzel, Joachim M.; Buhrmester, Hartmut; Straetling, Wolf H. [Reprint author]

CS Institut fuer Physiologische Chemie, Universitaets-Krankenhaus Eppendorf, Martinistrasse 52, 20246 Hamburg, Germany

SO Molecular and Cellular Biology, (1997) Vol. 17, No. 9, pp. 5656-5666. CODEN: MCEBD4. ISSN: 0270-7306.

DT Article

LA English

ED Entered STN: 8 Oct 1997
Last Updated on STN: 8 Oct 1997

AB Here, we describe the cloning and further characterization of chicken ARBP, an abundant nuclear protein with a high affinity for MAR/SARs. Surprisingly, ARBP was found to be homologous to the rat

protein MECP2, previously identified as a methyl-CpG-binding protein. A region spanning 125 amino acids in the N-terminal halves is 96.8% identical between chicken ARBP and rat MeCP2. A deletion mutation analysis using Southwestern and band shift ass vs identified this highly conserved region as the MAR DNA binding domain. Alignment of chicken ARBP with rat and human MeCP2 proteins revealed six trinucleotide amplifications generating up to 34-fold repetitions of a single amino acid. Because MeCP2 was previously localized to pericentromeric heterochromatin in mouse chromosomes, we analyzed the in vitro binding of ARBP to various repetitive sequences. In band shift experiments, ARBP binds to two chicken repetitive sequences as well as to mouse satellite DNA with high affinity similar to that of its binding to chicken lysozyme MAR fragments. In mouse satellite DNA, use of several footprinting techniques characterized two high-affinity binding sites, whose sequences are related to the ARBP binding site consensus in the chicken lysozyme MAR (5'-GGTGT-3'). Band shift experiments indicated that methylation increased in vitro binding of ARBP to mouse satellite DNA two- to fivefold. Our results suggest that ARBP/MeCP2 is a multifunctional protein with roles in loop domain organization of chromatin, the structure of pericentromeric heterochromatin, and DNA methylation.

L14 ANSWER 20 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 9

AN 1997:204550 BIOSIS

DN PREV199799503753

TI Transgenic expression of a CD46 (membrane cofactor protein) minigene: Studies of xenotransplantation and measles virus infection.

AU Thorley, Bruce R. [Reprint author]; Milland, Julie; Christiansen, Dale; Lanteri, Marc B.; McInnes, Beth; Moeller, Ingid; Rivailler, Pierre; Horvat, Branka; Rabourdin-Combe, Chantal; Gerlier, Denis; McKenzie, Ian F. C.; Loveland, Bruce E.

CS The Austin Res. Inst., Studley Road, Heidelberg, VIC 3084, Australia

SO European Journal of Immunology, (1997) Vol. 27, No. 3, pp. 726-734.

CODEN: EJIMAF. ISSN: 0014-2980.
DT Article
LA English
ED Entered STN: 12 May 1997
Last Updated on STN: 12 May 1997
AB CD46 (membrane cofactor protein) is a human cell-surface regulator of activated complement and a receptor for the measles virus. A CD46 transgenic mouse line with an expression pattern similar to that of human tissues has been produced, to develop an animal model of (i) the control of complement activation by complement regulators in hyperacute rejection of xenografts, and (ii) measles virus infection. The mouse line was made using a CD46 minigene that includes promoter sequence and the first two introns of genomic CD46, which was coinjected into mouse ova with chicken lysozyme matrix attachment region DNA. A high level of CD46 expression in homozygotic transgenic mice was obtained with spleen cells having approximately 75% of the level found on human peripheral blood mononuclear cells. CD46 was detected in all tissues examined by immunohistochemistry, radioimmunoassay and Western blotting, showing that these mice were suitable for transplantation and measles virus infection studies. It also indicated that the transgene included the important regulatory elements of the CD46 promoter. Transgenic spleen cells were significantly protected in vitro from human complement activated by either the classical or alternative pathways and from alternative pathway rat complement. Furthermore, transgenic mouse hearts transplanted to rats regulated complement deposition in an in vivo model of antibody-dependent hyperacute xenograft rejection. Similar to human lymphocytes, transgenic lymphoblasts could be infected in vitro with measles virus; infected cells expressed viral proteins and produced infectious viral particles. The data demonstrate the suitability of this minigene for obtaining high-level CD46 expression sufficient for enhanced resistance of transgenic cells to complement

attack and for obtaining wide tissue distribution of CD46, analogous to human tissues and, therefore, useful for comparative studies.

L14 ANSWER 21 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 10
AN 1997:454265 BIOSIS
DN PREV199799753468
TI Dissection of a synthesized quantitative trait to characterize transgene interactions.
AU Nap, Jan-Peter [Reprint author]; Conner, Anthony J.; Mlynarova, Ludmila; Stiekema, Willem J.; Jansen, Ritsert C.
CS Dep. Mol. Biol., CPRO-DLO, PO Box 16, NL-6700 AA Wageningen, Netherlands
SO Genetics, (1997) Vol. 147, No. 1, pp. 315-320.
CODEN: GENTAE. ISSN: 0016-6731.
DT Article
LA English
ED Entered STN: 27 Oct 1997
Last Updated on STN: 27 Oct 1997
AB Six transgenic tobacco lines, each homozygous for the beta-glucuronidase (GUS) gene at a different locus, and wild type were selfed and intercrossed to evaluate GUS activity in all possible hemizygous, homozygous and dihybrid combinations of GUS alleles. The transgenic lines are characterized by their GUS activity (two low, three intermediate, one high), T-DNA complexity (four single-copy, two more complex single-locus) and the presence of the chicken lysozyme matrix-associated region (MAR) around the full T-DNA (two lines). Gene action and interaction was analyzed by weighted linear regression with parameters for additivity, dominance and epistasis. The analysis showed that each of the four single-copy lines acted fully additively. In contrast, the two complex single-locus lines showed classical single-locus overdominance and were epistatic dominant over all other GUS alleles. The latter is manifested in severe suppression of GUS activity in dihybrid lines, irrespective of the presence of MAR elements around the GUS gene. Such elements apparently do not protect against epistatic dominance. The quantitative data suggested that the epistatic

dominance and overdominance are based on the same molecular mechanism.
Our approach of a genetic analysis of quantitative variation in well-characterized transgenic lines provides a powerful tool to gain insight into complex plant traits.

L14 ANSWER 22 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 11
AN 1996:461804 BIOSIS
DN PREV199699184160
TI Dissection of the ability of the chicken lysozyme gene 5' matrix attachment region to stimulate transgene expression and to dampen position effects.
AU Phi-Van, Loc; Straetling, Wolf H. [Reprint author]
CS Inst. fuer Physiologische Chemie, Universitaets-Krankenhaus Eppendorf, Martinistrasse 52, 20246 Hamburg, Germany
SO Biochemistry, (1996) Vol. 35, No. 33, pp. 10735-10742.
CODEN: BICHAW. ISSN: 0006-2960.
DT Article
LA English
ED Entered STN: 11 Oct 1996
Last Updated on STN: 11 Oct 1996
AB The chicken lysozyme gene domain is flanked by nuclear matrix attachment regions (MARS) on each side. We have previously shown that bilaterally flanking 5' MARS in stably transfected artificial genetic units enhance expression of a reporter transgene and dampen position effects of the chromatin structure at the site of integration. The 5' MAR was now dissected into smaller fragments that were monitored for effects on transgene expression in mouse 3T3 cells by a similar assay. Fragments, which contain 1.32 and 1.45 kb and represent the upstream and the downstream half, respectively, of the 5' MAR, retained the ability to stimulate transgene expression as well as the ability to reduce the variation in the level of expression. However, a 452 bp subfragment (H1-HaeII), which still exhibits specific binding to nuclear matrices and contains two high-affinity binding sites for the abundant nuclear matrix protein ARBP, lost both of those abilities. A dimerized 177 bp sequence from fragment H1-HaeII, which also binds selectively to nuclear matrices

and includes a duplicated ARBP binding site, was also unable to stimulate reporter gene expression. Furthermore, a 0.65 kb subfragment containing an intrinsically bent sequence did not affect an elevated reporter gene expression and its dampening. Our results show that the ability of MAR fragments to bind to nuclear matrices is not sufficient to enhance and insulate transgene expression in stably transfected cells.

L14 ANSWER 23 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 12
AN 1996:377536 BIOSIS
DN PREV199699099892
TI The chicken lysozyme gene 5' MAR and the Drosophila histone SAR are electroelutable from encapsulated and digested nuclei.
AU Hempel, Katrin; Straetling, Wolf H. [Reprint author]
CS Inst. Physiol. Chem., Univ. Krankenhaus Eppendorf, Martinistrasse 52, 20246 Hamburg, Germany
SO Journal of Cell Science, (1996) Vol. 109, No. 6, pp. 1459-1469. CODEN: JNCSAI. ISSN: 0021-9533.
DT Article
LA English
ED Entered STN: 26 Aug 1996
Last Updated on STN: 26 Aug 1996
AB Cultured chicken cells were encapsulated in agarose microbeads, lysed in a near-physiological buffer and resulting encapsulated nuclei were digested with a restriction enzyme and electroeluted. After removal of apprx 97% of the chromatin, the nuclear lamina, residual nucleoli and an internal nuclear network remained. The majority of nascent RNA was also recovered in digested and electroeluted nuclei. Surprisingly, however, the chicken lysozyme gene 5' MAR was quantitatively electroeluted from digested nuclei of expressing and non-expressing cells, as well as the promoter region and the coding sequence. When encapsulated nuclei were digested partially, the proportion of elutable 5' MAR chromatin was comparable to that of elutable bulk chromatin. Furthermore, after digestion of encapsulated nuclei from

Drosophila Kc cells, the histone SAR was electroeluted to the same extent as bulk chromatin. We conclude that the lysozyme gene 5' MAR and the histone SAR are not permanently attached to a nuclear matrix or scaffold.

L14 ANSWER 24 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1996:654094 CAPLUS
DN 125:298101
OREF 125:55743a,55746a
TI Effects of EHS matrix on expression of transgenes in HC11 cells
AU Lee, T. H.; Baik, M. G.; Im, W. B.; Lee, C. S.; Han, Y. M.; Kim. S. J.; Lee, K. K.; Choi, Y. J.
CS Coll. Agric. Sci. Technol., Seoul Natl. Univ., Seoul, 441-744, S. Korea
SO In Vitro Cellular & Developmental Biology: Animal (1996), 32(8), 454-456
CODEN: IVCAED; ISSN: 1071-2690
PB Society for In Vitro Biology
DT Journal
LA English
AB Culture of the mammary gland epithelial cell line HC11 on EHS (Engelbreth Holm Swarma) matrix resulted in the formation of 3-dimensional alveoli-like structures and the induction of expression of the endogenous whey acidic protein (WAP) gene and a WAP-human lactoferrin (hLF) hybrid gene. In addition, the chicken lysozyme 5' matrix attachment region (MAR) increased transcription of the WAP-hLF hybrid genes in HC11 cells. Thus, HC11 cells grown on EHS matrix could be used to study the WAP promoter and for WAP hybrid gene expression, especially when the transgenes are flanked by MARs.

L14 ANSWER 25 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1997:550025 CAPLUS
DN 127:230318
OREF 127:44811a,44814a
TI Chicken lysozyme gene 3' matrix attachment regions did not activate transfected gene expression in homologous cells
AU Xu, Hanhua; Phi-van, Loc
CS Inst. Anim Sci., CAAS, Beijing, 100094, Peop. Rep. China
SO Zhongguo Shouyi Xuebao (1996), 16(3), 212-217
CODEN: ZSXUF5; ISSN: 1005-4545
PB Zhongguo Shouyi Xuebao Bianjibu
DT Journal
LA Chinese
AB Matrix attachment regions (MARs) have been identified in several genes.

Nuclear MARs in genomic DNA are thought to be involved in nearly all important processes of the nucleus, for instance, the organization of chromatin loop-domains, DNA replication, DNA repairing; RNA transcription and processing. The MARs of the chicken lysozyme gene were identified at the boundaries of the "active" chromatin domain. The MAR element located 5' of the chicken lysozyme gene has been shown to mediate elevated, position-less dependent expression of genes which stably transfected into chicken or heterologous cells. Here, chicken HD11 cells were stably transfected either with a construct (EPC) containing the chicken lysozyme gene enhancer (E) and promoter (P) fused to the reporter gene (C) encoding bacterial chloramphenical acetyl transferase (CAT) gene or with the constructs (MEPCM, MEPC, EPCM) in which EPC transcription units were flanked by chicken lysozyme gene 3' MAR. In this system, the 3' MAR from the chicken lysozyme gene could not activate the expression of transfected genes in homologous cells.

L14 ANSWER 26 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 13

AN 1995:265410 BIOSIS
DN PREV199598279710
TI Nuclear Matrix Protein ARBP Recognizes a Novel DNA Sequence Motif and High Affinity.
AU Buhrmester, Hartmut; Von Kries, Jens P.; Straetling, Wolf H. [Reprint author]
CS Inst. Physiol. Chem., Univ. Krankenhaus Eppendorf, Martinistrasse 52, 20246 Hamburg, Germany
SO Biochemistry, (1995) Vol. 34, No. 12, pp. 4108-4117. CODEN: BICHAW. ISSN: 0006-2960.
DT Article
LA English
OS DDBJ-X84223; EMBL-X84223; Genbank-X84223
ED Entered STN: 26 Jun 1995
Last Updated on STN: 26 Jun 1995
AB ARBP is a nuclear protein that specifically binds to matrix/scaffold attachment regions (MARs/SARs). Here we characterize by DNase I footprinting, dimethyl sulfate protection, and mobility shift assays two

binding sites for ARBP within a chicken lysozyme
MAR fragment. Our results indicate that ARBP recognizes a novel
DNA sequence motif containing the central sequence 5'-GGTGT-3' and
flanking AT-rich sequences. Binding occurs through major groove contacts
to two guanines of the central sequence. Collective and single-base
substitutions in the 5'-GGTGT-3' core motif result in loss or significant
reductions of ARBP binding, underscoring the importance of the GC-rich
core sequence. Structural elements of the sequence motif are probably
also recognized. The affinity of ARBP to both binding sites is
surprisingly high (K-D = (2-6) times 10-10 M). High-affinity recognition
of the identified DNA motif in MARs/SARs by ARBP is likely an important
feature in the domain organization of chromatin.

L14 ANSWER 27 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN DUPLICATE 14
AN 1994:159413 BIOSIS
DN PREV199497172413
TI The rat probasin gene promoter directs hormonally and developmentally
regulated expression of a heterologous gene specifically to the prostate
in transgenic mice.
AU Greenberg, N. M. [Reprint author]; Demayo, F. J.; Sheppard, P. C.;
Barrios, R.; Lebovitz, R.; Finegold, M.; Angelopoulou, R.; Dodd, J. G.;
Duckworth, M. L.; Rosen, J. M.; Matusik, R. J.
CS Dep. Cell Biology, Baylor Coll. Med., Houston, TX 77030, USA
SO Molecular Endocrinology, (1994) Vol. 8, No. 2, pp. 230-239.
CODEN: MOENEN. ISSN: 0888-8809.
DT Article
LA English
ED Entered STN: 8 Apr 1994
Last Updated on STN: 10 Apr 1994
AB An expression cassette carrying 426 basepairs of the rat probasin (PB)
gene promoter and 28 basepairs of 5'-untranslated region is sufficient to
target the expression of the bacterial chloramphenicol acetyltransferase
(CAT) gene specifically to the prostate in transgenic mice. The PS-CAT
transgene was expressed in three of five (60%) independent lines of mice,

and this expression, as reported previously for the endogenous rat gene, was male specific, restricted primarily to the lateral, dorsal, and ventral lobes of the prostate, with only very low levels Of CAT activity detected in the anterior prostate and seminal vesicles. The developmental and hormonal regulation of the transgene also paralleled that reported for the rat gene, with a 70-fold increase in CAT activity in the mouse prostate observed between 2-7 weeks of age, a time corresponding to sexual maturation. PB-CAT activity in the prostate declined after castration to 3.5% of the precastration level, and the CAT activity in castrated males approached precastration levels when mice were supplemented with testosterone. Transgene expression in castrated males was not induced by dexamethasone. Coinjection of PB-CAT with a chicken lysozyme gene matrix attachment region resulted in their cointegration and further restricted the pattern of PB-CAT to the dorsolateral prostate, with suppressed expression observed in the ventral prostate. These studies demonstrate that a minimal rat probasin promoter can target heterologous gene expression specifically to the prostate in a developmentally and hormonally regulated fashion.

L14 ANSWER 28 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1992:544725 CAPLUS
DN 117:144725
OREF 117:24953a,24956a
TI Matrix-attachment regions can impart position-independent regulation of a tissue-specific gene in transgenic mice
AU McKnight, Robert A.; Shamay, Avi; Sankaran, Lakshmanan; Wall, Robert J.; Hennighausen, Lothar
CS Lab. Biochem. Metab., Natl. Inst. Diabetes Dig. Kidney Dis., Bethesda, MD, 20982, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1992), 89(15), 6943-7
CODEN: PNASA6; ISSN: 0027-8424
DT Journal

LA English
AB Matrix-attachment regions (MARs) may function as domain boundaries and
partition chromosomes into independently regulated units. The authors
tested whether MAR sequences from the chicken lysozyme locus,
the so-called A-elements, can confer position-independent regulation to a
whey acidic protein (WAP) transgene in mammary tissue of mice. In the
absence of MARs, expression of WAP transgenes was observed in 50% of the
lines, and regulation during pregnancy, during lactation, and upon
hormonal induction did not mimic that of the endogenous WAP gene and
varied with the integration site. In contrast, all 11 lines in which WAP
transgenes were juxtaposed to MAR elements showed expression. Accurate
position-independent hormonal and developmental regulation was seen in
four out of the five lines analyzed. These results indicate that MARs can
establish independent genetic domains in transgenic mice.
OSC.G 141 THERE ARE 141 CAPLUS RECORDS THAT CITE THIS RECORD (141 CITINGS)

L14 ANSWER 29 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on
STN DUPLICATE 15
AN 1990:425736 BIOSIS
DN PREV199090086537; BA90:86537
TI A NON-CURVED CHICKEN LYSOZYME 5' MATRIX ATTACHMENT SITE IS 3'
FOLLOWED BY A STRONGLY CURVED DNA SEQUENCE.
AU VON KRIES J P [Reprint author]; PHI-VAN L; DIEKMANN S; STRAETLING W H
CS INSTITUT FUER PHYSIOLOGISCHE CHEMIE, UNIVERSITAETS-KRANKENHAUS EPPENDORF,
MARTINISTRASSE 52, D-2000 HAMBURG 20, FRG
SO Nucleic Acids Research, (1990) Vol. 18, No. 13, pp. 3881-3386.
CODEN: NARHAD. ISSN: 0305-1048.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 22 Sep 1990
Last Updated on STN: 22 Sep 1990
AB Matrix attachment regions (MARs) partition the genome into functional and
structural loop-domains. Here, we determined the relative matrix affinity
of cloned fragments of the chicken lysozyme 5'

MAR. We show that this region contains a non-curved high-affinity binding site, which is 3' followed by a strongly curved DNA sequence that exhibits weak matrix binding. DNA curvature is not a physical property required for strong matrix binding. Possible biological functions of this sequence arrangement, particularly of the strongly curved DNA, are discussed.

L14 ANSWER 30 OF 31 BIOSIS COPYRIGHT (c) 2009 The Thomson Corporation on STN DUPLICATE 16
AN 1990:261579 BIOSIS
DN PREV199090003665; BA90:3665
TI THE CHICKEN LYSOZYME 5' MATRIX ATTACHMENT REGION INCREASES TRANSCRIPTION FROM A HETEROLOGOUS PROMOTER IN HETEROLOGOUS CELLS AND DAMPENS POSITION EFFECTS ON THE EXPRESSION OF TRANSFECTED GENES.
AU PHI-VAN L [Reprint author]; VON KRIES J P; OSTERTAG W; STRAETLING W H
CS INST PHYSIOLOGISCHE CHEM, UNIV-KRANKENHAUS EPPENDORF, FRG
SO Molecular and Cellular Biology, (1990) Vol. 10, No. 5, pp. 2302-2307.
CODEN: MCEBD4. ISSN: 0270-7306.
DT Article
FS BA
LA ENGLISH
ED Entered STN: 5 Jun 1990
Last Updated on STN: 6 Jun 1990
AB Matrix attachment regions (MARs) are DNA elements that dissect the genome into topologically separated domains by binding to a chromosomal skeleton. This study explored the putative influence of the MAR located 5' of the chicken lysozyme gene on expression of heterologous genes in heterologous cell systems. Expression of a construct with the chloramphenicol acetyltransferase (CAT) indicator gene controlled by the herpes simplex virus thymidine kinase promoter (TC) and a construct in which the same transcriptional unit is flanked by chicken lysozyme 5' MARs (MTCM) was assayed after stable transfection into rat fibroblasts. Median CAT activity per copy number in MTCM transfectants was elevated approximately 10-fold relative to that in TC transfectants.

Total variation in normalized CAT activity decreased from more than
100-fold among TC transfectants to nearly 6-fold among MTCM transfectants.
The steady-state level of transcripts and the relative rate of transcription were increased in MTCM transfectants, as shown by S1
nuclease and run-on transcription assays, respectively. The chicken lysozyme 5' MAR thus can confer
elevated, less position-dependent expression on a heterologous promoter in
cells of a different species by increasing the density of transcribing RNA
polymerase molecules. MAR-mediated transcriptional enhancment suggests
that MARs are important for gene expression and not just for DNA packaging.

L14 ANSWER 31 OF 31 CAPLUS COPYRIGHT 2009 ACS on STN
AN 1991:95897 CAPLUS
DN 114:95897
OREF 114:16215a,16218a
TI The chicken lysozyme 5' matrix
attachment region increases transcription from a
heterologous promoter in heterologous cells and dampens position effects
on the expression of transfected genes
AU Stein, Arnold
CS Purdue Univ., West Lafayette, IN, USA
SO Chemtracts: Biochemistry and Molecular Biology (1990), 1(5), 434-7
CODEN: CMBIE5; ISSN: 1045-2680
DT Journal; General Review
LA English
AB The title research of L. Phi-Van, et al. (1990) is reviewed with commentary and 12 refs.

=> FIL STNGUIDE

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	104.54	317.65

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	-11.48	-21.32

FILE 'STNGUIDE' ENTERED AT 18:03:22 ON 21 OCT 2009

FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Oct 16, 2009 (20091016/UP).

=>

---Logging off of STN---

=>
Executing the logoff script...

=> LOG Y

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.28	317.93

DISCOUNT AMOUNTS (FOR QUALIFYING ACCOUNTS)	SINCE FILE ENTRY	TOTAL SESSION
CA SUBSCRIBER PRICE	0.00	-21.32

STN INTERNATIONAL LOGOFF AT 18:05:55 ON 21 OCT 2009